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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:44:25 ; Search time 468 Seconds

(without alignments)
59.188 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113

Sequence: 1 MRRMKSLLAALTYGAMLAAPVATA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 Seqs, 1107998698 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 0%
Listing First 45 summaries

Database : Pending Patents AA Main.*
1: /cggn2_6/ptodata/1/paa/us03—"COMB.pep;*"

2: /cggn2_6/ptodata/1/paa/us06—"COMB.pep;*"

3: /cggn2_6/ptodata/1/paa/us07—"COMB.pep;*"

4: /cggn2_6/ptodata/1/paa/us08—"COMB.pep;*"

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8: /cggn2_6/ptodata/1/paa/us04—"COMB.pep;*"

9: /cggn2_6/ptodata/1/paa/us05—"COMB.pep;*"

10: /ggn2_6/ptodata/1/paa/us06—"COMB.pep;*"

11: /cggn2_6/ptodata/1/paa/us08—"COMB.pep;*"

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25: /cggn2_6/ptodata/1/paa/us09—"COMB.pep;*"

26: /ggn2_6/ptodata/1/paa/us10—"COMB.pep;*"

27: /cggn2_6/ptodata/1/paa/us11—"COMB.pep;*"

28: /cggn2_6/ptodata/1/paa/us12—"COMB.pep;*"

29: /cggn2_6/ptodata/1/paa/us13—"COMB.pep;*"

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31: /cggn2_6/ptodata/1/paa/us15—"COMB.pep;*"

32: /cggn2_6/ptodata/1/paa/us16—"COMB.pep;*"

33: /cggn2_6/ptodata/1/paa/us17—"COMB.pep;*"

34: /cggn2_6/ptodata/1/paa/us18—"COMB.pep;*"

35: /cggn2_6/ptodata/1/paa/us19—"COMB.pep;*"

36: /cggn2_6/ptodata/1/paa/us60—"COMB.pep;*"

Result No.	Score	Query	Match	Length	DB ID	Description
1	113	100.0	25	27	US-10-112-488-2	Sequence 2, Appli
2	113	100.0	25	32	US-10-173-860-3	Sequence 3, Appli
3	57	50.4	295	21	US-09-738-626-644	Sequence 6644, Appli
4	57	50.4	395	34	US-10-805-394-6644	Sequence 6644, Appli
5	56	49.6	135	26	US-10-015-127-11477	Sequence 11497, Appli
6	55	48.7	517	30	US-10-149-902-42629	Sequence 42629, Appli
7	55	48.7	526	30	US-10-137-962-19030	Sequence 19030, Appli
8	52	46.0	141	22	US-09-791-537-76056	Sequence 76056, Appli
9	51.5	45.6	87	27	US-10-156-761-12894	Sequence 12894, Appli
10	51	45.1	104	21	US-09-738-626-4865	Sequence 4865, Appli
11	51	45.1	104	34	PCT-US99-03265-84	Sequence 84, Appli
12	51	45.1	107	1	PCT-US99-03268-83	Sequence 83, Appli
13	51	45.1	107	10	US-08-658-800-84	Sequence 84, Appli
14	51	45.1	107	10	US-08-659-683-83	Sequence 83, Appli
15	51	45.1	107	10	US-08-660-573-84	Sequence 84, Appli
16	51	45.1	107	10	US-08-660-573-83	Sequence 83, Appli
17	51	45.1	107	11	US-08-723-622-84	Sequence 84, Appli
18	51	45.1	107	11	US-08-730-510-83	Sequence 83, Appli
19	51	45.1	107	13	US-08-912-341-84	Sequence 83, Appli
20	51	45.1	107	13	US-08-925-578-83	Sequence 83, Appli
21	51	45.1	107	14	US-09-024-753-84	Sequence 84, Appli
22	51	45.1	107	14	US-09-025-197-83	Sequence 83, Appli
23	51	45.1	107	21	US-09-724-685-83	Sequence 83, Appli
24	51	45.1	107	26	US-10-084-843-83	Sequence 84, Appli
25	51	45.1	107	26	US-10-194-002-84	Sequence 84, Appli
26	51	45.1	168	1	PCT-US99-03265-95	Sequence 95, Appli
27	51	45.1	168	1	PCT-US99-03268-100	Sequence 100, Appli
28	51	45.1	168	1	PCT-US99-03268-100	Sequence 94, Appli
29	51	45.1	168	10	US-08-658-900-94	Sequence 100, Appli
30	51	45.1	168	10	US-08-659-683-100	Sequence 94, Appli
31	51	45.1	168	10	US-08-680-573-94	Sequence 100, Appli
32	51	45.1	168	10	US-08-680-574-100	Sequence 94, Appli
33	51	45.1	168	11	US-08-723-622-94	Sequence 100, Appli
34	51	45.1	168	11	US-08-730-510-100	Sequence 95, Appli
35	51	45.1	168	13	US-08-942-341-95	Sequence 100, Appli
36	51	45.1	168	13	US-08-942-578-100	Sequence 95, Appli
37	51	45.1	168	14	US-09-024-753-95	Sequence 100, Appli
38	51	45.1	168	14	US-09-025-197-100	Sequence 100, Appli
39	51	45.1	168	21	US-09-724-685-100	Sequence 100, Appli
40	51	45.1	168	26	US-10-009-384-19	Sequence 19, Appli
41	51	45.1	168	26	US-10-080-170-534	Sequence 534, Appli
42	51	45.1	168	26	US-10-084-843-100	Sequence 100, Appli
43	51	45.1	168	27	US-10-193-002-95	Sequence 534, Appli
44	51	45.1	168	30	US-10-468-356-534	Sequence 64, Appli
45	51	45.1	187	1	PCT-US99-03265-64	Sequence 64, Appli

ALIGNMENTS

RESULT 1
US-10-112-488-2
; Sequence 2, Application US/10112488
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Yoshihini
; ATTORNEY: DATE, Masayo
; APPLICANT: UMEZAWA, Yukiko
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: MATSUI, Hiroshi
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
; FILE REFERENCE: 219286US000NT
; CURRENT APPLICATION NUMBER: US/10/112,488
; PRIORITY APPLICATION NUMBER: 2003-04-01
; PRIORITY FILING DATE: 2003-04-01
; PRIORITY FILING DATE: 2000-09-29
; PRIORITY APPLICATION NUMBER: JP2000-280098
; PRIORITY FILING DATE: 2000-06-28
; PRIORITY APPLICATION NUMBER: JP11-280098
; NUMBER OF SEQ ID NOS: 70

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Corynebacterium ammoniagenes
US-10-112-488-2

Query Match Score 113; DB 27; Length 25;
Best Local Similarity 100.0%; Pred. No. 1. 6e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAGAMILAAPVATA 25
Db 1 MKRMKSLAAALTVAGAMILAAPVATA 25

RESULT 2
US-10-673-860-3
SEQUENCE 3 Application US/10673860
GENERAL INFORMATION:
APPLICANT: Ajinomoto Co., Inc.
TITLE OF INVENTION: A method of secreting and producing proteins
FILE REFERENCE: Y1J0182
CURRENT APPLICATION NUMBER: US/10/673,860
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: JP 2001-98808
PRIOR FILING DATE: 2001-03-30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 25
TYPE: PRT
ORGANISM: Corynebacterium ammoniagenes
US-10-673-860-3

Query Match Score 113; DB 32; Length 25;
Best Local Similarity 100.0%; Pred. No. 1. 6e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAGAMILAAPVATA 25
Db 1 MKRMKSLAAALTVAGAMILAAPVATA 25

RESULT 3
US-09-738-626-6644
SEQUENCE 6644, Application US/09738626
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: OCHIAI, AKIKO
APPLICANT: HAYASHI, MIKIRO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/10/805,394
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: JP 99-377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/155162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
ORGANISM: Corynebacterium glutamicum
US-10-805-394-6644

Query Match Score 57; DB 34; Length 395;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRMKSIAAALTVAGAMILA 19
Db 13 KRUKPLAAAVAVAGVLLA 30

RESULT 4
US-10-805-394-6644
SEQUENCE 6644, Application US/10805394
GENERAL INFORMATION:
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/805,394
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: JP 99-377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/155162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
ORGANISM: Corynebacterium glutamicum
US-10-805-394-6644

Query Match Score 57; DB 34; Length 395;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRMKSIAAALTVAGAMILA 19
Db 13 KRUKPLAAAVAVAGVLLA 30

RESULT 5
US-10-015-127-11497
SEQUENCE 11497, Application US/10015127
GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: *Sphingomonas elodea* genome sequences and uses thereof
FILE REFERENCE: 38-10-(15806)B
CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NO: 14357
SEQ ID NO 11497
LENGTH: 135
TYPE: PRT
ORGANISM: *Sphingomonas elodea*
US-10-015-127-11497

Query Match Score 57; DB 34; Length 395;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRMKSIAAALTVAGAMILA 19
Db 13 KRUKPLAAAVAVAGVLLA 30

RESULT 6
US-09-738-626-6644
SEQUENCE 6644, Application US/09738626
GENERAL INFORMATION:
APPLICANT: OZAKI, AKIO
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99-377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NO: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 395
LENGTH: 395
TYPE: PRT

Query Match 49.6%; Score 56; DB 26; Length 135;
 Best Local Similarity 54.5%; Pred. No. 5.5;
 Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0; Gaps 0;

Qy :||: MKSLAAALTVAGMLAAPVATA 25
 Db :||: MKTILATLIGALLANAVANA 22

RESULT 6
 US-10-449-902-42629
 ; Sequence 42629, Application US/10449902
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203229
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 42629
 ; LENGTH: 517
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-42629

Query Match 48.7%; Score 55; DB 30; Length 517;
 Best Local Similarity 54.2%; Pred. No. 36;
 Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0; Gaps 0;

Qy :||: KRMKSLAAALTVAGMLAAPVATA 25
 Db :||: RRRSRRAAVVVALILLASAATA 29

RESULT 7
 US-10-437-963-190930
 ; Sequence 190930, Application US/10437963
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 18-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 190930
 ; LENGTH: 526
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)...(526)
 ; OTHER INFORMATION: unsure at all xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_87298C.1.pep
 ; US-10-437-963-190930

Query Match 48.7%; Score 55; DB 30; Length 526;

Query Match 54.2%; Score 54.2%; DB 27; Length 87;
 Best Local Similarity 54.2%; Pred. No. 16;
 Matches 15; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy :||: MKSLAAALTVAGMLAAPVATA 25
 Db :||: MESSLAKAAAVVAGSMVLAGAVAPA 23

RESULT 8
 US-09-791-537-76056
 ; Sequence 76056, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danner, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 76056
 ; LENGTH: 141
 ; TYPE: PRT
 ; ORGANISM: Streptomyces aureofaciens
 ; US-09-791-537-76056

Query Match 46.0%; Score 52; DB 22; Length 141;
 Best Local Similarity 47.8%; Pred. No. 24;
 Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy :||: RMKSLAAALTVAGMLAAPVATA 25
 Db :||: RLVALAGAAAATVLIAGPVAAA 28

RESULT 9
 US-10-156-761-12894
 ; Sequence 12894, Application US/10156761
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHITAKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-362
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO: 12894
 ; LENGTH: 87
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 ; US-10-156-761-12894

Query Match 45.6%; Score 51.5; DB 27; Length 87;
 Best Local Similarity 65.2%; Pred. No. 16;
 Matches 15; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy :||: MESSLAAALTVAGMLAAPVATA 25
 Db :||: MESSLAKAAAVVAGSMVLAGAVAPA 23

RESULT 10

US-09-738-626-4865
 Sequence 4865, Application US/09738626
 GENERAL INFORMATION:
 APPLICANT: NAKAGAWA, SATOSHI
 APPLICANT: MIZOGUCHI, HIROSHI
 APPLICANT: ANDO, SEIKO
 APPLICANT: HAYASHI, MIKIRO
 APPLICANT: OCHIAI, KEIKO
 APPLICANT: YOKOI, HARUHIKO
 APPLICANT: TATEISHI, NAOKO
 APPLICANT: SENOH, AKIHIRO
 APPLICANT: IKEDA, MASATO
 APPLICANT: OZAKI, AKIO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 CURRENT APPLICATION NUMBER: US/09/738,626
 CURRENT FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: JP 99/377484
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: JP 00/159162
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: JP 00/280988
 PRIOR FILING DATE: 2000-04-03
 SOFTWARE: PatentIn ver. 3.0
 SEQ ID NO 4865
 LENGTH: 104
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-4865

Query Match 45.1%; Score 51; DB 21; Length 104;
 Best Local Similarity 48.0%; Pred. No. 24;
 Matches 12; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGRMKSLAAATVAGMLAAAPVATA 25
 Db 2 IKKYLTIAAVTIAASAVLFAPSQA 26

RESULT 12
 PCT-US99-03265-84
 Sequence 84, Application PC/TUS9903265
 GENERAL INFORMATION:
 APPLICANT: Coixa Corporation
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 TUBERCULOSIS
 NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds, LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-8811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US99/03265
 FILING DATE: 17-FEB-1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/024,753
 FILING DATE: 18-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Laura A. Coruzzi
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 9532-0023-228
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 PCT-US99-03265-84

Query Match 45.1%; Score 51; DB 1; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MGRMKSLAAATVAGMLAA 20
 Db 10 MGRMKSLAAATVAGMLAAIGRA 29

RESULT 13
 PCT-US99-03266-83
 Sequence 83, Application PC/TUS9903266
 GENERAL INFORMATION:
 APPLICANT: Coixa Corporation
 TITLE OF INVENTION: AND DIAGNOSTS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds, LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York

Query Match 45.1%; Score 51; DB 34; Length 104;
 SEQ ID NO 4865
 LENGTH: 104
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-10-805-394-4865

COUNTRY: USA
 ZIP: 10036-2811
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US99/03268
 FILING DATE: 17-FEB-1999
 CLASSIFICATION: 406
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/025,197
 FILING DATE: 18-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Cottizzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 9332-0013-228
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US99-03268-83

Query Match 45.1% ; Score 51; DB 1; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTVAGAMIAA 20
 Db 1.0 MKMVKSIAGLTAAGAA 29

RESULT 14
 US-08-658-800-84
 Sequence 84, Application US/08658800
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 123
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/658,800
 FILING DATE: 05-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-658-83-83

RESULT 16
 US-08-680-573-84
 Sequence 84, Application US/08680573
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonia
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:

RESULT 15
 US-08-659-683-83
 Sequence 83, Application US/08659683
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 128
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659,683
 FILING DATE: 05-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-659-683-83

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 128
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/680,573
 FILING DATE: 12-JUL-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-0314
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear

US-08-680-573-84

Query Match 45.1%; Score 51; DB 10; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMKSLAALTYAGMLAA 20
 Db 10 MKVYKSIAGLTAANIGAA 29

RESULT 18
 US-08-729-622-84

Query Match 45.1%; Score 51; DB 10; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMKSLAALTYAGMLAA 20
 Db 10 MKVYKSIAGLTAANIGAA 29

RESULT 19
 US-08-729-622-84

Query Match 45.1%; Score 51; DB 10; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMKSLAALTYAGMLAA 20
 Db 10 MKVYKSIAGLTAANIGAA 29

RESULT 18
 US-08-729-622-84

Sequence 94, Application US/08729622
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vediwick, Thomas H.
 APPLICANT: Twardzik, David R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 NUMBER OF SEQUENCES: 132
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/729,622
 FILING DATE: 11-OCT-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-0314
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear

US-08-729-622-84

Query Match 45.1%; Score 51; DB 11; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMKSLAALTYAGMLAA 20
 Db 10 MKVYKSIAGLTAANIGAA 29

RESULT 17
 US-08-680-574-83

Sequence 83, Application US/08680574
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 133
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/680,574
 FILING DATE: 12-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-0314
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear

US-08-729-622-84

Query Match 45.1%; Score 51; DB 11; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMKSLAALTYAGMLAA 20
 Db 10 MKVYKSIAGLTAANIGAA 29

RESULT 19
 US-08-730-510-83
 / Sequence 93, Application US/08730510
 / GENERAL INFORMATION:
 / APPLICANT: Reed, Steven G.
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Campos-Neto, Antonio
 / APPLICANT: Houghton, Raymond
 / APPLICANT: Vediuk, Thomas S.
 / APPLICANT: Twardzik, Daniel R.
 / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 / NUMBER OF SEQUENCES: 137
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: SEED and BERRY LLP
 / STREET: 6300 Columbia Center, 701 Fifth Avenue
 / CITY: Seattle
 / STATE: Washington
 / ZIP: 98104-7012
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/730,510
 / FILING DATE: 27-AUG-1996
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Maki, David J.
 / REGISTRATION NUMBER: 31,392
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (206) 622-4900
 / TELEFAX: (206) 682-6031
 / US-08-730-510-83
 / Query Match 45.1%; Score 51; DB 11; Length 107;
 / Best Local Similarity 60.0%; Pred. No. 24;
 / Matches 12; Conservative 3; Mismatches 5; Indels 0;
 / Gaps 0;
 /
 RESULT 20
 US-08-942-341-84
 / Sequence 84, Application US/08942341
 / GENERAL INFORMATION:
 / APPLICANT: Reed, Steven G.
 / APPLICANT: Skeiky, Yasir A.M.
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Campos-Neto, Antonio
 / APPLICANT: Houghton, Raymond
 / APPLICANT: Vediuk, Thomas S.
 / APPLICANT: Twardzik, Daniel R.
 / APPLICANT: Lods, Michael J.
 / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 / NUMBER OF SEQUENCES: 209
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: SEED and BERRY LLP
 / STREET: 6300 Columbia Center, 701 Fifth Avenue
 / CITY: Seattle
 / STATE: Washington
 / ZIP: 98104-7092
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/942,578
 / FILING DATE: 01-OCT-1997
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Maki, David J.
 / REGISTRATION NUMBER: 31,392
 / REFERENCE/DOCKET NUMBER: 210121.411C7
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (206) 622-4900

STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/942,341
 FILING DATE: 01-OCT-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-942-341-84
 Query Match 45.1%; Score 51; DB 13; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0;
 Gaps 0;
 Qy 1 MKRMKSLAAALTYAGAMLA 20
 Db 10 MKMVKSIAGLTAAAIGAA 29
 /
 RESULT 21
 US-08-942-578-83
 / Sequence 83, Application US/08942578
 / GENERAL INFORMATION:
 / APPLICANT: Reed, Steven G.
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Campos-Neto, Antonio
 / APPLICANT: Houghton, Raymond
 / APPLICANT: Vediuk, Thomas S.
 / APPLICANT: Twardzik, Daniel R.
 / APPLICANT: Lods, Michael J.
 / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 / NUMBER OF SEQUENCES: 214
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: SEED and BERRY LLP
 / STREET: 6300 Columbia Center, 701 Fifth Avenue
 / CITY: Seattle
 / STATE: Washington
 / ZIP: 98104-7092
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/942,578
 / FILING DATE: 01-OCT-1997
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Maki, David J.
 / REGISTRATION NUMBER: 31,392
 / REFERENCE/DOCKET NUMBER: 210121.411C7
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (206) 622-4900

US-09-025-197-83
 TELEFAX: (206) 682-5031
 INVENTION: SEQUENCE FOR SEQ ID NO: 83;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-942-578-83
 Query Match 45.1%; Score 51; DB 13; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAALTVAGAMLA 20
 Db 10 MKMVKSIAGLTAAAGGA 29

RESULT 22
 US-09-024-753-84
 Sequence 84, Application US/C9024753
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 241
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,197
 FILING DATE: 18-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-025-197-83
 Query Match 45.1%; Score 51; DB 14; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAALTVAGAMLA 20
 Db 10 MKMVKSIAGLTAAAGGA 29

RESULT 24
 US-09-724-685-83
 Sequence 83, Application US/09724685
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 TITLE OF INVENTION: Compounds and Methods for Immunotherapy and Diagnosis of Tuberculosis
 NUMBER OF SEQUENCES: 155
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/724,685
 FILING DATE: 28-NOV-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/523,436
 FILING DATE: 01-SEP-1995
 APPLICATION NUMBER: US 08/533,634
 FILING DATE: 22-SEP-1995
 APPLICATION NUMBER: US 08/620,874
 FILING DATE: 22-MAR-1996
 APPLICATION NUMBER: US 08/659,683
 FILING DATE: 05-JUN-1996
 APPLICATION NUMBER: US 08/680,574
 FILING DATE: 12-JUL-1996
 APPLICATION NUMBER: WO PCT/US96/14674
 FILING DATE: 30-AUG-1996
 APPLICATION NUMBER: US 08/730,511
 FILING DATE: 11-OCT-1996
 APPLICATION NUMBER: US 08/618,112
 FILING DATE: 13-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Baustian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 014058-008561US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 83:
 US-09-724-685-83

Query Match 45.1%; Score 51; DB 21; Length 107;
 Best Local Similarity 60.0%; Prd. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MKRMKSLAAALTYAGAMLA 20
 || :||:|| | :|| | :|| | :|| |
 Db 10 MKMVKSIAGLTAAAIGAA 29

RESULT 25

US-10-084-843-83
 Sequence 83, Application US/10084843
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.

Shreiky, Yasir A.W.
 Dillon, Davin C.
 Campos-Neto, Antonio
 Houghton, Raymond
 Vedrick, Thomas S.
 Twardzik, Daniel R.
 Lodes, Michael J.

Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 TUBERCULOSIS

NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/193,002
 FILING DATE: 10-Jul-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 ATTORNEY/AGENT INFORMATION:

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/084,843
 FILING DATE: 25-Feb-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,967
 ATTORNEY/AGENT INFORMATION:
 NAME: Mati, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121-411C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 83:
 US-10-084-843-83
 Query Match 45.1%; Score 51; DB 26; Length 107;
 Best Local Similarity 60.0%; Prd. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MKRMKSLAAALTYAGAMLA 20
 || :||:|| | :|| | :|| |
 Db 10 MKMVKSIAGLTAAAIGAA 29
 RESULT 26
 US-10-193-002-84
 Sequence 84, Application US/10193002
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.

Shreiky, Yasir A.W.
 Dillon, Davin C.
 Campos-Neto, Antonio
 Houghton, Raymond
 Vedrick, Thomas S.
 Twardzik, Daniel R.
 Lodes, Michael J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

TUBERCULOSIS

NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/193,002
 FILING DATE: 10-Jul-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-10-193-002-84

SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Query Match 45.1%; Score 51; DB 27; Length 107;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 MRMKSLAAALTVAGMLAA 20

Db 10 MRMKSLAAALTVAGMLAAIGAA 29

RESULT 27
 PCT-US99-032265-95
 Sequence 95, Application PC/US99/032265
 GENERAL INFORMATION:
 APPLICANT: Corixa Corporation
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 TITLE OF INVENTION: TUBERCULOSIS
 NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESS: Pennie & Edmonds, LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: USA
 COUNTRY: USA

PRIORITY INFORMATION:

APPLICATION NUMBER: US 09/024,753
 FILING DATE: 18-FEB-1998
 ATTORNEY/AGENT INFORMATION:

NAME: Laura A. Coruzzi
 REGISTRATION NUMBER: 30,742
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

PCT-US99-032265-95

Query Match 45.1%; Score 51; DB 1; Length 168;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 MRMKSLAAALTVAGMLAA 20

Db 1 MRMKSLAAALTVAGMLAAIGAA 29

RESULT 28
 PCT-US99-03268-100
 Sequence 100, Application PC/US99/03268
 GENERAL INFORMATION:
 APPLICANT: Corixa Corporation
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds, LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

PRIORITY INFORMATION:

APPLICATION NUMBER: US 09/025,197
 FILING DATE: 18-FEB-1998
 ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura, A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 9532-0013-228

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

PCT-US99-03268-100

Query Match 45.1%; Score 51; DB 1; Length 168;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 MRMKSLAAALTVAGMLAA 20

Db 1 MRMKSLAAALTVAGMLAAIGAA 29

RESULT 29
 PCT-US99-03265-95
 Sequence 94, Application US/08658800
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiry, Yasir A.W.
 APPLICANT: Dillon, Devin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 NUMBER OF SEQUENCES: 123
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

Query Match 45.1%; Score 51; DB 1; Length 168;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 MRMKSLAAALTVAGMLAA 20

Db 1 MRMKSLAAALTVAGMLAAIGAA 29

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/658, 800
 FILING DATE: 05-JUN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4940
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-558-800-94

Query Match Best Local Similarity 45.1%; Score 51; DB 10; Length 168;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVGAMLLA 20
 Db 1 MKRVSIAAGLTAAAGAA 20

RESULT 30
 US-08-659-683-100
 Sequence 100, Application US/08659683
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 128
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659, 683
 FILING DATE: 05-JUN-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-680-573-94

Query Match Best Local Similarity 45.1%; Score 51; DB 10; Length 168;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTVGAMLLA 20
 Db 1 MKRVSIAAGLTAAAGAA 20

RESULT 31
 US-08-680-573-94
 Sequence 94, Application US/08680573
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCE: 128
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle

Query Match Best Local Similarity 45.1%; Score 51; DB 10; Length 168;

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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,574
FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
STRANDEDNESS: single
TOPOLOGY: Linear
US-08-680-574-100

RESULT 33
Query Match      45.1%;  Score 51;  DB 10;  Length 168;
Best Local Similarity 60.0%;  Pred. No. 41;
Matches 12;  Conservative 3;  Mismatches 5;  Indels 0;  Gaps 0;
Qy   1 MKRMKSIAALTYAGAMLA 20
Db   1 MKMVKSIAAGLTAAAIGGA 20

US-08-729-622-94
Sequence 94, Application US/08729622
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond H.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,622
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
US-08-730-510-100

Query Match      45.1%;  Score 51;  DB 11;  Length 168;
Best Local Similarity 60.0%;  Pred. No. 41;
Matches 12;  Conservative 3;  Mismatches 5;  Indels 0;  Gaps 0;
Qy   1 MKRMKSIAALTYAGAMLA 20
Db   1 MKMVKSIAAGLTAAAIGGA 20

RESULT 35
US-08-942-341-95

```

Sequence 95, Application US/08942341
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Veddick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 209
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/942,578
 FILING DATE: 01-OCT-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 IN INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-942-578-100

Query Match Score 51; DB 13; Length 168;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTAGAMLA 20
 Db 1 MKYVKSIAAGLTAAGAAGA 20

RESULT 37
 US-08-942-578-95
 Sequence 95, Application US/09024753
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Veddick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 236
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/024,753
 FILING DATE: 18-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 IN INFORMATION FOR SEQ ID NO: 95:
 SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-024-753-95

Query Match Score 51; DB 14; Length 168;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLA 20
 Db 1 MKMVKSIAGLTTAAAIGGA 20

RESULT 38
 US-09-025-197-100
 Sequence 100, Application US/09025197
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Twardzik, Daniel J.
 APPLICANT: Lodes, Michael J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/724,685
 FILING DATE: 28-Nov-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/523,436
 FILING DATE: 01-SEP-1995
 APPLICATION NUMBER: US 08/533,634
 FILING DATE: 22-SEP-1995
 APPLICATION NUMBER: US 08/620,874
 FILING DATE: 22-MAR-1996
 APPLICATION NUMBER: US 08/659,683
 FILING DATE: 05-JUN-1996
 APPLICATION NUMBER: US 08/680,574
 FILING DATE: 12-JUL-1996
 APPLICATION NUMBER: WO PCT/US96/14674
 FILING DATE: 30-AUG-1996
 APPLICATION NUMBER: US 08/730,511
 FILING DATE: 11-OCT-1996
 APPLICATION NUMBER: US 08/818,112
 FILING DATE: 13-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Bachtar, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 014058-008561US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 100:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-025-197-100

Query Match Score 51; DB 14; Length 168;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLA 20
 Db 1 MKMVKSIAGLTTAAAIGGA 20

RESULT 40
 US-10-009-384-19
 Sequence 19, Application US/10009384
 GENERAL INFORMATION:
 APPLICANT: Gennaro, Maria Laura
 APPLICANT: Gomez, Manuel J.
 TITLE OF INVENTION: SECRETED PROTEINS OF MYCOBACTERIUM

RESULT 39
 US-09-724-685-100
 Sequence 100, Application US/09724685

TITLE OF INVENTION: TUBERCULOSIS AND THEIR USE AS VACCINES AND DIAGNOSTIC
TITLE OF INVENTION: REAGENTS
FILE REFERENCE: 07763-042001
CURRENT APPLICATION NUMBER: US/10/009,384
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: US 60/132,503
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: US 60/132,479
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 94
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 19
LENGTH: 168
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-009-384-19

Query Match Score 51; DB 26; Length 168;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Oy 1 MRCRMKSIAAALTYAGAMIAA 20
Db 1 MRNIVKSIAGLITAAIGAA 20

Search completed: December 1, 2004, 11:59:31
Job time : 469 secs

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GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: December 1, 2004, 11:33:34 ; Search time 189 Seconds
 (without alignments)
 76.108 Million cell updates/sec

Title: US-10-673-860-3
 Perfect score: 113
 Sequence: 1 MIRMKSLAAALTVAGAMLAAPVATA 25

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:
 1: uniprot_sprot:
 2: uniprot_trembl:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	113	100.0	358	2	Q93R90	corynebacter
2	57	50.4	385	2	Q6M204	corynebacter
3	57	50.4	385	2	CAP20877	corynebac
4	57	50.4	395	2	Q8N1TS	corynebacter
5	56	50.4	430	2	Q8A4C2	cellvibrio
6	56	49.6	346	2	Q7NXL7	chromobacte
7	54	47.8	438	2	Q6SH08	Q6sh08 uncultured
8	53	47.8	438	2	AAR37811	Aar37811 unculture
9	53	46.9	122	2	Q71618	Q71618 mycobacteri
10	53	46.9	122	2	AAQ12134	AAQ12134 mycobacter
11	53	46.9	133	2	Q9YG03	Q9yg03 aeropyrum p
12	53	46.9	333	2	Q8FK93	Q8fk9 bradyrhizob
13	53	46.9	507	2	O50506	O50506 streptomyce
14	52	46.0	141	1	RNS3_STRAU	P3289 streptomyce
15	52	46.0	399	2	Q985D9	Q95d9 rhizobium 1
16	51.5	45.6	87	2	Q93HK7	streptomyce
17	51.5	45.6	948	2	QBQLQ7	QBqlq7 saccharopol
18	51	45.1	104	2	QBNR31	QBnr31 corynebac
19	51	45.1	104	2	CAP1936	CAP1936 corynebac
20	51	45.1	168	1	MB12_MYCTU	003822 mycobacteri
21	51	45.1	248	2	Q8XVA4	Q8va4 ralstonia s
22	51	45.1	431	2	Q9S3L6	Q9s3l6 bacillus sp
23	51	45.1	434	2	054327	054327 bacillus sp
24	51	45.1	482	2	QBXTE9	QBxte9 ralstonia s
25	50.5	44.7	328	2	Q7W382	Q7w382 bordetella
26	50.5	44.7	328	2	Q7WEKL	Q7wekl bordetella
27	50	44.2	81	2	Q829D3	Q829d3 streptomyce
28	50	44.2	100	2	Q9KYG9	Q9kyg9 streptomyce
29	50	44.2	125	1	RL7_RICPR	Q9se21 rickettsia
30	50	44.2	279	2	Q8NTB4	Q8ntb4 corynba
31	50	44.2	313	2	CAF19108	CAF19108 corynba

ALIGNMENTS

RESULT 1		PRT7	
Q93R90	ID	Q93R90;	PRELIMINARY;
	AC	Q93R90;	
	DT	01-DBC-2001 (TREMBLrel.	19, Created)
	DT	01-DBC-2001 (TREMBLrel.	19, Last sequence update)
	DT	01-TUN-2002 (TREMBLrel.	21, Last annotation update)
	DB	Cell surface Protein A.	
	GN	Name=cspA;	
	OS	Corynebacterium ammoniagenes (Brevibacterium ammoniagenes).	
	OC	Bacteria; Actinobacteria; Actinomycetales;	
	OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
	OX	NCBI_TaxID=1637;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	STRAIN=ATCC 6572;	
	RA	Usuda Y., Kawasaki H., Utagawa T.;	
	RA	nCharacterization of the cell surface protein gene of Corynebacterium ammoniagenes.	
	RT	RT ammoniagenes.	
	RL	Biochim. Biophys. Acta 1552:138-141 (2001).	
	DR	EMBL; AB055224; BAB62413; -.	
	DR	InterPro; IPR000801; Esterase,_Put.	
	DR	Pfam; PF00756; Esterase_1.	
	RX	[1]	
	RT	mature cell surface protein A.	
	QT	SEQUENCE 358 AA; 0185CA6602311A1_CRC67;	
	CHAIN	26 358 mature cell surface protein A.	
	SEQUENCE	358 AA; 39001 MW;	
	QY	1 MKRMKSLAAALTVAGMLAAPVATA 25	
	Db	1 MKRMKSLAAALTVAGMLAAPVATA 25	
RESULT 2		PRT; 385 AA.	
Q6M204	ID	Q6M204;	PRELIMINARY;
	AC	Q6M204;	
	DT	05-JUL-2004 (TREMBLrel.	27, Created)
	DT	05-JUL-2004 (TREMBLrel.	27, Last sequence update)
	DT	05-JUL-2004 (TREMBLrel.	27, Last annotation update)
	DE	BETA-N-ACETYLGLUCOSAMINIDASE (EC 3.2.1.52).	
	GN	Name=nagaZ2; OrderedLocusNames=cg3158;	
	OS	Corynebacterium glutamicum (Brevibacterium flavum).	
	OC	Bacteria; Actinobacteria; Actinomycetales;	
	OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
	OX	NCBI_TaxID=1718;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;	
	RX	PubMed:12948626;	
	RA	Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,	
	RA	Eikmanns B.J., Gaigalat L., Burkova A., Disch N., Eggeling L.,	

RA	Goessmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moekkel B., Pfeiffer W., Puehler A., Rey D.A., Rueckert C., Rupp O., Salm H., Wendisch V.F., Wiegraebe I., Tauch A.; "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.",	DN GN OS OC OC OX RN RP RC RA RT RN SEQUENCE FROM N.A. STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa; Nakagawa S.;
DR	EMBL; BX92156; CAEP0877.1; -.	RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032." Submitted (MAY-2002) to the EMBL/CenBank/DDBJ databases. EMBL; AP005283; BAC00246.1; -.
GO	GO:00016798; P:hydrolase activity, acting on glycosyl bonds; IEA.	DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR	GO:0001764; Glyco_hydro_3N.	DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR	IntersPro; IPR001764; Glyco_hydro_3.1.	DR InterPro; IPR001764; Glyco_hydro_3N.
DR	Pfam; PF00933; Glycosidase; Hydrolase.	DR Pfam; PF00933; Glycosidase; Hydrolase.
KW	SEQUENCE 385 AA;	KW Complete proteome; Glycosidase; Hydrolase.
SO	SEQUENCE 385 AA; 40473 MW; 367F80C810D53849 CRC64;	SO 395 AA; PFB35F878C4F064D CRC64;
Query Match	Score 57; DB 2; Length 385;	Query Match Score 57; DB 2; Length 395;
Best Local Similarity	50.4%; Pred. No. 16;	Best Local Similarity 66.7%; Pred. No. 16;
Matches	12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy	2 KRMKSLAAALTAGAMLA 19	Qy 2 KRMKSLAAALTAGAMLA 19
Db	3 KRLKPILAAAVAVAGVLLA 20	Db 13 KRLKPILAAAVAVAGVLLA 30
RESULT 3		RESULT 5
CAF20877	PRELIMINARY;	Q840C2
ID	CAF20877	ID
AC	CAF20877; PRELIMINARY;	PRELIMINARY;
DT	02-MAR-2004 (TREMBLrel. 27, Created)	AC
DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)	DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)	DT 01-MAR-2004 (TREMBLrel. 24, Last sequence update)
DE	BETA-N-ACETYLGLUCOSAMINIDASE (EC 3.2.1.52).	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
GN	NAGA2 OR NG3158.	DE Endo-b1,4-mannanase 5A.
OS	Corynebacterium glutamicum (Brevibacterium flavum)	GN Name-mana5A;
OC	Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;	OS Cellvibrio japonicus.
OC	Corynebacteriae; Corynebacteriaceae; Corynebacterium.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
NCBI_TaxID=1718;		OC Pseudomonadaceae; Cellvibrio.
RN	SEQUENCE FROM N.A.	NCBI_TaxID=155077;
RP	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;	RN [1] -
RA	Kalinowski J., Bathke B., Bartels D., Bischoff N., Bott M., Burkovski A., Dussek N., Eggeling L., Eikmanns B.J., Gaigalat L., Goessmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moekkel B., Pfeiffer W., Puehler A., Rey D.A., Rueckert C., Rupp O., Salm H., Wendisch V.F., Wiegraebe I., Tauch A.;	RP SEQUENCE FROM N.A. PubMed=12523937;
RT	"The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.",	RX MEDLINE=22588103; PubMed=12523937;
RT	Tauch A.; "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.",	RA Hogg D., Pell G., Dupre P., Goubet F., Martin-Orue S.M., Armand S., Gilbert H.J.;
RA	J. Biotechnol. 104:5-25(2003). EMBL; BX92156; CAEP0877.1; -.	RT "The modular architecture of Cellvibrio japonicus mannanases in glycoside hydrolase families 5 and 26 points to differences in their role in mannose degradation."
DR	SEQUENCE 385 AA; 40473 MW; 367F80C810D53849 CRC64;	RL Biochem. J. 371:1027-1043 (2003). EMBL; AV187031; AAO31759.1; -.
DR	GLYCOSIDASE; Hydrolase.	DR HSSP; PI4768; 1E8R.
DR	GO:0005975; F:carbohydrate metabolism; IEA.	DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR	InterPro; IPR009031; CBDX.	DR InterPro; IPR009031; CBDX.
DR	InterPro; IPR002833; Dockerin_CBD_5.	DR InterPro; IPR001547; Glyco_hydro_5.
DR	Pfam; PF002013; CBM 10; 2.	DR Pfam; PF00150; Cellulase; 1.
DR	PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN 1.	DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN 1.
SQ	SEQUENCE 385 AA; 40473 MW; 367F80C810D53849 CRC64;	SQ SEQUENCE 430 AA; AE55FEB0A9B073F CRC64;
Query Match	Score 57; DB 2; Length 385;	Query Match Score 57; DB 2; Length 430;
Best Local Similarity	50.4%; Pred. No. 16;	Best Local Similarity 54.2%; Pred. No. 18;
Matches	12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy	2 KRMKSLAAALTAGAMLA 19	Qy 2 KRMKSLAAALTAGAMLA 25
Db	3 KRLKPILAAAVAVAGVLLA 20	Db 24 RIKITLVAGLTAGLMMAAVSARA 47
RESULT 4		RESULT 6
Q8NLNT5	PRELIMINARY;	
ID	Q8NLNT5;	
AC	Q8NLNT5; PRELIMINARY;	
DT	01-OCT-2002 (TREMBLrel. 22, Created)	
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	

Q7NXL7	PRELIMINARY;	PRT;	346 AA.		RP SEQUENCE FROM N.A. DeLong E.F.; RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases. RN [2]
AC Q7NXL7;	26; Created)				
DT 01-MAR-2004 (TREMBLrel. 26; Last sequence update)					
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)					
DT Peptidoglycan N-acetyl-muramoylhydrolase (EC 3.2.1.17).					
DE Chromobacter; Order=LocusNames=cv1609;					
GN Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;					
OS Chromobacterium violaceum.					
OC Neisseriaceae; Chromobacterium.					
OX NCBI_TaxID=36;					
RN [1]	SEQUENCE FROM N.A.				
RP STRAIN=ATCC 12472 / DSM 30191;					
RC MEDLINE=228828800 PubMed=14500782;					
RX PROSITE; PS50850; MFS; 1.					
RX PROSITE; PS0016; SUGAR_TRANSPORT_1; UNKNOWN_1.					
RX PROSITE; PS0017; SUGAR_TRANSPORT_2; UNKNOWN_1.					
RA Antonio R.V., Almeida F.C., de Almeida R., Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F., Astolfo-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M., Baptista J.S., Belo A., van den Berg C., Bogo M., Bonatto S., Bordignon J., Brigido M.M., Brito C.A., Broccchi M., Burity H.A., Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carrasco D.M., Carvalho C.M.B., Cascudo J.C.M., Cavada B.S., Chueire L.M.O., Creczynski-Pasa T.B., Cunha-Junior N.C., Falcão C.L., Ferreira M.I.T., Franco G.R., Freitas N.S.A., Ferro J.A., Fanticatti P., Farias I.P., Felipe M.R., Ferriari L.P., Ferro J.A., Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangiero T.B., Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J., Leitão L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P., Mafeira H.M.F., Manfio G.P., Maranhão R., Martins W.S., Mauricio S.M.Z., de Medeiros A.Q., Moreira R.V., Moreira M.A.M., Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C., Paixaos R.F.C., Parente J.A., Perner J.O., Pena S.D.J., Pereira J.O., Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P., Ranallo-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E., Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N., Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simões I.C., Simón D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L., Souza R.C., Steffens M.B.R., Steinidel M., Teixeira S.R., Urmenyi T., Vettore A., Wassem R., Zahia A., Simpson A.J.G.;	RESULT 8	AAR37811	PRELIMINARY; PRT;	438 AA.	
RA	"The complete genome sequence of Chromobacterium violaceum reveals remarkable and exploitable bacterial adaptability."				
RA	Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003). EMBL: A5016915; AAQ59285.1.				
DR GO:0016798; P: Hydrolase activity, acting on glycosyl bonds; IEA.					
DR GO:0003796; P: Lysozyme activity; IEA.					
DR GO:0005975; P: carbohydrate metabolism; IEA.					
DR Complete protease activity; IEA.					
DR Glycosidase, Hydrolase.					
DR Hydrolase activity, acting on glycosyl bonds; IEA.					
DR	SEQUENCE 346 AA; 38077 MW; EFC981BC371B172 CRC44;				
SQ	Query Match Score 56; DB 2; Length 346; Best Local Similarity 56.0%; Pred. No. 20; Matches 14; Conservative 1; Mismatches 10; Indels 0; Gaps 0;				
Qy 1 MKRMKSLAAALTYAGAMMLAPVATA 25					
Db 1 MKSMKLATAAALAGAALTAPPQA 25					
RESULT 7					
Q6SH08	PRELIMINARY;	PRT;	438 AA.	RESULT 9	
TD Q6SH08;				Q716L8	
AC Q6SH08;	27; Created)			ID Q716L8;	PRELIMINARY;
DT 05-JUL-2004 (TREMBLrel. 27; Last sequence update)				AC Q716L8;	PRT;
DT 05-JUL-2004 (TREMBLrel. 27; Last annotation update)				DT 05-JUL-2004 (TREMBLrel. 27; Last sequence update)	
DT 05-JUL-2004 (TREMBLrel. 27; Last annotation update)				DT 05-JUL-2004 (TREMBLrel. 27; Last annotation update)	
DR Vanillate transporter VanK, putative.				DR GP57.	
GN uncultured bacterium 443.				OS Mycobacteriophage PG1.	
OS uncultured bacterium environmental samples.				OC Virus; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.	
OC NCBITaxonID=257393;				NCBI_TaxID=2132326;	
RN [1]				OX	

[1]

EN SEQUENCE FROM N.A.
RP Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RA Pedulla M.L., Ford M.E., Houtz J.M., Hendrix R.W.;
RL EMBL; AF547430; AAQ12134;1-.
SQ SEQUENCE 122 AA; 13339 MW; F55AACED7F5AFF71 CRC64;

Query Match 46.9%; Score 53; DB 2; Length 122;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 12; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

Qy 2 KRMKS-LAAALTVAGAMLAAPVATA 25
Db 3 RRLKALAAVAMTAAGGALATAPAASA 28

RESULT 10
ID AAQ12134 PRELIMINARY; PRT; 122 AA.
AC 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Gp57.
OS Mycobacteriophage PG1.
OC dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=213236;
RN [1]

RP SEQUENCE FROM N.A.
RA Hatfull G.F., Pedulla M.L., Ford M.E., Houtz J.M., Hendrix R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF547430; AAQ12134;1-.
SQ SEQUENCE 122 AA; 13339 MW; F55AACED7F5AFF71 CRC64;

Query Match 45.9%; Score 53; DB 2; Length 122;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 12; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

Qy 2 KRMKS-LAAALTVAGAMLAAPVATA 25
Db 3 RRLKALAAVAMTAAGGALATAPAASA 28

RESULT 11
ID Q9YG03 PRELIMINARY; PRT; 133 AA.
AC 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 133aa long hypothetical eukaryotic Ig lambda-1 chain V region.
DE OrderedLocusNames=APE0098;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
NCBI_TaxID=566336;
RN

RP SEQUENCE FROM N.A.
RC STRAIN=KL;
SQ MEDLINE=99310339; PubMed=10382966;

Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
Jin-no R., Takahashi M., Sekine M., Baba S.-I., Aikai A., Kosugi H.,
Hosoya A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Mysuda S., Furashashi T., Tanaka F., Kudou Y.,
Yamazaki J., Kusida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kiruchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, *Aeropyrum pernix* K1.";
EMBL; AP000058; BAA79007.1; -.
PIR; E72763; E72763.
KW Complete proteome; Hypothetical protein.

SEQUENCE FROM N.A.
RP STRAIN=N3 (2) / M145; RC

[1]

EN SEQUENCE FROM N.A.
RP Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RA RMKS-LAAALTVAGAMLAAPVATA 25
SQ SEQUENCE 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Query Match 46.9%; Score 53; DB 2; Length 133;
Best Local Similarity 56.5%; Pred. No. 25;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RMKS-LAAALTVAGAMLAAPVATA 25
Db 9 KMQSPKAALTAGSSSNAPATA 31

RESULT 12
ID Q89FK9 PRELIMINARY; PRT; 333 AA.
AC Q89FK9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-MAR-2004 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Thiosulfate sulfurtransferase.
OrderedLocusNames=bhl6620;
OS Bradyrhizobium japonicum ";
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=USA110;
SQ MEDLINE=2484998; PubMed=12597275;

Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Iesawa K., Iriuchi M., Kawashima K.,
Kohata M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
"Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005959; BAC51955;1-.
HSSP; P00586; 1 RHS
DR GO:0004794; Fl thiolsulfate sulfurtransferase activity; IEA.
DR GO:0016740; Fl transferase activity; IEA.
DR GO:0008272; Fl sulfate transport; IEA.
DR InterPro; IPR011763; Rhodanese-like.
DR InterPro; IPR01307; Thiolsulftrans.
PFam; PF00581; Rhodanese; 2.
SMART; SM04450; RHOD; 2.
PROSITE; PS00380; RHODANESE_1; 1.
PROSITE; PS50206; RHODANESE_3; 2.
KW Complete proteome; Transferase; Transferase; Sequence
SEQUENCE 333 AA; CD3989P36946FB43 CRC64;

Query Match 46.9%; Score 53; DB 2; Length 333;
Best Local Similarity 48.0%; Pred. No. 50;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MKRMS-LAAALTVAGAMLAAPVATA 25
Db 264 MKPLDDLRRAFTGAGVLDAPIVTS 288

RESULT 13
ID 050306 PRELIMINARY; PRT; 507 AA.
AC 050306;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative secreted chitinase (Putative secreted protein).
GN OrderedLocusNames=SCG0012; ORFNames=SC7B7.09c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyctaceae; Streptomyces.
NCBI_TaxID=1902;
RN

RP SEQUENCE FROM N.A.
RC STRAIN=N3 (2) / M145; RC

RE MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentler K.F., Chater K.F., Cerdeno-Tarrega A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RR EMBL; AL939126; CAA15789; 1.; -.
 DR PIR; T55677; T35577.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0030246; F:carbohydrate binding; IEA.
 DR GO; GO:00016787; F:hydrolase activity; IEA.
 DR GO; GO:0004533; F:hydrolase activity; IEA.
 DR GO; GO:0005935; F:carbohydrate metabolism; IEA.
 DR GO; GO:0008152; F:metabolism; IEA.
 DR InterPro; IPR003410; CBM_5_12.
 DR InterPro; IPR001223; Glyco_hydro_18.
 DR Pfam; PF002839; CRM_5_12.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR SMART; SM00195; ChtBD; 1.
 KW Complete proteome;
 SEQUENCE 507 AA; 52681 MW; 5EAD34A9874C6A73 CRC64;

Query Match 46.9%; Score 53; DB 2; Length 507;
 Best Local Similarity 55.0%; Prod. No. 70; 0;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTYAGAMLA 20
 Db 1 MRRRSIRRALTAATTVA 20

RESULT 14
 RNS3 STRAU STANDARD; PRT; 141 AA.
 ID _RNS3 STRAU STANDARD; PRT; 141 AA.
 AC P30789; 1.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Guanyl-specific ribonuclease Sa3 precursor (EC 3.1.27.3) (RNase Sa3).
 GN Name=rnasa3;
 OS Streptomyces aureofaciens.
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Streptomycineae; Streptomyctaceae; Streptomyces.
 RN [1] NCBI_TaxID=1894;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10762 / CCM 3239;
 RM MEDLINE=93012368; PubMed=1398084;
 RA Homerova D., Holasenderova Z., Kormanec J., Sevcik J.;
 RT "Cloning and sequencing of the gene encoding a ribonuclease from
 Streptomyces aureofaciens CCM3239."; Gene 119:147-148 (1992).
 RL [2]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 45-141.
 RA Pubmed=12228255; DOI=10.1074/jbc.M20845200;
 RT Sevcik J., Urbanikova L., Leland P.A., Raines R.T.;
 RT "X-ray structure of two crystalline forms of a streptomycte
 ribonuclease with cytotoxic activity.";
 RL J. Biol. Chem. 277:47325-47330 (2002)
 CC -: CATALYTIC ACTIVITY: Two-stage endonucleolytic cleavage to
 nuclease 3'-phosphoglycerides ending in
 G-P with 2',3'-cyclic phosphate intermediates.
 CC -: SUBCELLULAR LOCATION: Secreted.
 CC -: SIMILARITY: Belongs to the ribonuclease N1/rl family.
 CC -: CAUTION: Ref.1 sequence differs from that shown due to
 frameshifts.

RESULT 15
 Q985D9 PRELIMINARY; PRT; 399 AA.
 ID Q985D9 PRELIMINARY; PRT; 399 AA.
 AC Q985D9; 1.
 DT 01-OCT-2001 (T-EMBLrel. 18, Created)
 DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE ABC transporter, binding protein.
 GN OrderedLocusNames=mLR727;
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alpha-proteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OC NCBI_TaxID=381;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=MAFF303059;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanaabe A., Iida K., Kawashima A., Ishikawa A., Kohara M., Matsuno A.,
 RA Kishida Y., Kiyosawa C., Matsunoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Tabata S., Sugimoto M.,
 RA Takeuchi C., Yanai M.,
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti".
 RL DNA Res. 7:331-338 (2000).

RA Tauch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins";
 RT J. Biotechnol. 104: 5-25 (2003).
 DR EMBL; AF05277; BAB98926.1; -.
 DR EMBL; BX927151; CAF1936.1; -.
 KW Complete proteome; Hypothetical protein;
 SEQUENCE 104 AA; 11121 MW; 03D2E5192615DD9E CRC64;

Query Match Score 51; DB 2; Length 104;
 Best Local Similarity 48.0%; Pred. No. 38; 8; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 8; Standard 0;
 SPECIES FROM N.A.

QY 1 MKRMKSLAAALTYAGMLAAPVATA 25
 :|: |: |: |: |: |: |:
 DB 2 IKKYLSTIAAVTASAVLFAPSQA 26

RESULT 19
 CAF19936 ID CAE19936 PRELIMINARY; PRT; 104 AA.
 AC CAP19936_0004 (TREMBrel. 27, Created)
 DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)
 DE Purative secreted protein.
 GN CGB1389.
 SPRAYN=ATCC 13032 / DSM 20300 / NCIB 10025;
 PubMed=12948526;
 RX RA Bischoff N., Bartels D., Bott M.,
 RA Burkhardt J., Bahe B., Eggeling L., Eikmanns B.J., Gaigalat L.,
 RA Goessmann A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
 RA Goessmann A., Hartmann M., Ruthmacher K., Kraemer R., Linke B.,
 RA Richard A.C., Meyer F., Moekel B., Peifferle W., Puehler A.,
 RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegraebe I.,
 RA Tauch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins";
 RT J. Biotechnol. 104: 5-25 (2003).
 DR EMBL; BX927151; CAF1936.1; -.
 SEQUENCE 104 AA; 11121 MW; 03D2E5192615DD9E CRC64;

Query Match Score 51; DB 2; Length 104;
 Best Local Similarity 48.0%; Pred. No. 38; 8; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 8; Standard 0;
 SPECIES FROM N.A.

QY 1 MKRMKSLAAALTYAGMLAAPVATA 25
 :|: |: |: |: |: |: |:
 DB 2 IKKYLSTIAAVTASAVLFAPSQA 26

RESULT 20
 MB12 MYCTU ID MB12_MYCTU STANDARD; PRT; 168 AA.
 AC 005522; PRT; 168 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Low molecular weight antigen MTB12 precursor (low molecular weight protein antigen 2) (CFP-2).
 GN Name=mtb12; Synonyms=cfp2; OrderedLocusNames=Rv2376c, MT2445, Mb2397c;
 GN Mycobacterium tuberculosis, and
 OS Mycobacterium bovis.
 OS Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriae; Mycobacterium.

01-JUN-2003 (TREMBurel, 24, Created)
 DT 01-JUN-2003 (TREMBurel, 24, Last sequence update)
 DT 01-OCT-2003 (TREMBurel, 25, Last annotation update)
 DE Putative secreted protein.
 OrderedLocusNames=SAV6478;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinomycetales; Streptomyces;
 NCBI_TaxID=33903;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX STRAIN=MA-4680;
 MEDLINE=22608206; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 microorganism Streptomyces avermitilis.";
 RL Biotechnol. 21:526-531(2003).
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC-31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osono T.,
 RA Kikuchi H., Shiba T., Sakai Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 avermitilis: deducing the ability of producing secondary
 metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
 DR EMBL;AP005046;BAC74189.1;-.
 DR InterPro;IPR05528;DUF320.-.
 DR Pfam;PF03777;DUF320;DUF320.-.
 KW Complete proteome.
 SEQUENCE 81 AA; 7630 MW; E0A2791CCCADF51D CRC64;
 Query Match 44.2%; Score 50; DB 2; Length 81;
 Best Local Similarity 44.0%; Pred. No. 43;
 Matches 11; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTYAGAMLAAPVATA 25
 Db 1 MSNLKKVAATVYAGGLVYAGAMA 25

RESULT 28
 Q9RYG9 PRELIMINARY; PRT; 100 AA.
 ID Q9RYG9; PRELIMINARY;
 AC Q9RYG9; PRELIMINARY;
 DT 01-OCT-2000 (TREMBurel, 15, Created)
 DT 01-OCT-2000 (TREMBurel, 15, Last sequence update)
 DT 01-MAR-2003 (TREMBurel, 23, Last sequence update)
 DE Purative membrane protein.
 GN OrderedLocusNames=SCC0703; ORFNames=SCC61A_24c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetales; Streptomyces;
 NCBI_TaxID=1902;
 RX SEQUENCE FROM N.A.
 MEDLINE=2199610; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 Huang C.-H., Kieser T., Larkie L., Murphy L.D., Oliver K., O'Neil S.,
 Rabinowitzsch B., Rajandream M.A., Rutledge K.M., Rutter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
 Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3 (2)." ;
 Nature 417:141-147 (2002).
 RL

DR EMBL; AL939113; CAB92269.1; -.
 KW Complete proteome;
 SQ SEQUENCE 100 AA; 9870 MW; 0D770E1D46F938A CRC64;
 Query Match 44.2%; Score 50; DB 2; Length 100;
 Best Local Similarity 64.7%; Pred. No. 50;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 MKSLAAALTYAGAMLA 20
 Db 1 MKSLKAAVAGSLVYA 17

RESULT 29
 RL7_RICPR STANDARD; PRT; 125 AA.
 ID RL7_RICPR
 AC Q9ZEJ1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 50S ribosomal protein L7/L12.
 GN Name=rpL11; Order=rediobcuhames-RP139;
 OS Rickettsia prowazekii.
 OC Bacteria; Protoplastacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid F;
 RX MEDLINE=98039499; PubMed=9823893; DOI=10.1038/24094;
 RA Andersson S.G.E., Zomerdorp A., Andersson J.O.,
 RA Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeelius A.K.,
 RA Briksson A.-S., Winkler H.H., Kurland C.G.;
 SQ "The Genome sequence of Rickettsia prowazekii and the origin of
 mitochondrial DNA";
 RT Nature 396:133-140(1998).
 RL Nature 396:133-140(1998).
 CC FUNCTION: Seems to be the binding site for several of the factors
 involved in protein synthesis and appears to be essential for
 accurate translation (By similarity).
 CC -1- SIMILARITY: Belongs to the Li2P family of ribosomal proteins.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and/or commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce>
 or send an email to licences@isb-sib.ch).
 CC
 CC DR EMBL; AU235270; CAA14607.1; -.
 CC DR PIR; H71723; H71733.
 CC DR HSSP; P29396; 1DD3.
 CC DR HAMAP; MF_00368; -; 1.
 CC DR InterPro; IPR002026; Ribosomal_L12.
 CC DR InterPro; IPR008932; Ribosomal_L12.
 CC DR Pfam; PF00542; Ribosomal_L12; 1.
 CC DR PRODom; PD001326; Ribosomal_L12; 1.
 CC DR TIGRFAMS; TIGR00855; L12; 1.
 CC DR Complete proteome; Ribosomal protein.
 SQ SEQUENCE 125 AA; 13213 MW; 431EDA82F25DB867 CRC64;

Query Match 44.2%; Score 50; DB 1; Length 125;
 Best Local Similarity 60.0%; Pred. No. 60;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 6 SIAAALTYAGAMLAAPVATA 25
 Db 33 SAAAAPITVAVAGYVAPLAEA 52

RESULT 30
 Q8NTB4 PRELIMINARY; PRT; 279 AA.
 ID Q8NTB4

AC Q8NTW9;	Query Match Score 50;	DB 2;	Length 279;
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	Best Local Similarity 44.2%;	Pred. No. 1.1e+02;	Gaps 0;
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)	Matches 12;	Conservative 2;	Mismatches 11; Indels 0;
DI 01-OCT-2004 (TREMBLrel. 28, Last annotation update)	Matches 12;	Conservative 2;	Mismatches 11; Indels 0;
DE Hypothetical membrane protein (Conserved secreted protein).	Score 50;	DB 2;	Length 279;
GN OrderdLocusName=Cg10393, cg0471;	Qy 1 MKRMKSLLAALTVALGAMLAAPVATA 25	Score 50;	DB 2;
OS Corynebacterium glutamicum (Brevibacterium flavum).	Db 1 MNRFPSALLAASVAGAAALAPVATA 25	Score 50;	DB 2;
OC Bacteria; Actinobacteria; Actinomycetales;	Qy 1 MKRMKSLLAALTVALGAMLAAPVATA 25	Score 50;	DB 2;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.	Db 1 MNRFPSALLAASVAGAAALAPVATA 25	Score 50;	DB 2;
OX NCBI_TaxID=1718;	Qy 1 MKRMKSLLAALTVALGAMLAAPVATA 25	Score 50;	DB 2;
RN [1]	Db 1 MNRFPSALLAASVAGAAALAPVATA 25	Score 50;	DB 2;
RP SEQUENCE FROM N.A. / DSM 20300 / NCIB 10025 Nakagawa;	Q92KJ0 PRELIMINARY;	PRT; 284 AA.	
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;	ID Q92KJ0 PRELIMINARY;	PRT; 284 AA.	
RA Nakagawa S.;	AC Q92KJ0 PRELIMINARY;	PRT; 284 AA.	
RT "Complete genomic sequence of <i>Corynebacterium glutamicum</i> ATCC 13032.";	DT 01-DBC-2001 (TREMBLrel. 19, Created)		
RU Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	DT 01-DBC-2001 (TREMBLrel. 19, Last sequence update)		
RN [2]	SEQUENCE FROM N.A. / DSM 20300 / NCIB 10025;	DB PUTATIVE OUTER MEMBRANE PROTEIN.	
RP SEQUENCE FROM N.A. / DSM 20300 / NCIB 10025;	GN OrderdLocusNames=002666; ORFNames=SMc02451;		
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;	OS Rhizobium meliloti (Sinorhizobium meliloti).		
RA PubMed:12948626;	CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;		
RA Kalinowski J., Bathé B., Bartels D., Bischoff N., Bott M., Gaiglak L.,	OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
RA Burkhardt A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,	QX NCBI_TaxID=388;		
RA McHardy A.-C., Meyer F., Moekel B., Pfefferle W., Puehler A.,	RN [1] _TAXID=388;		
RA Rey D.A., Rueckert C., Rupp O., Sähm H., Wendisch V.F., Wiegraebe I.,	RP SEQUENCE FROM N.A.		
RA Tauch A.;	RC STRAIN=1021;		
RA "The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins";	RX MEDLINE=21368234; PubMed=11474104;		
RR J. Biotechnol. 104:5-25(2003).	RA Galbert P., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barloy-Hubler F., Barnett M.J., Becker P., Boistard P., Bothie G., Cadieu E., Capela D., Chain P., Bourry M., Bowser L., Buhrmester J., Cadieu E., Dreano S., Fisher R.F., Cowie A., Davis R.W., Dreano S., Federspiel N.A., Golding B., Gouy J., Gurjal M., Gloux S., Godrie T., Goiffau A., Golding B., Hymann R.W., Jones T., Kahn D., Hernandez-Lucas I., Hong A., Huizink L., Kiss B., Komp C., Leaure V., Kahn M.L., Kalman S., Keating D.H., Kiss B., Portebeille D., Purnelle B., Kahn D., Palm C., Peck M.C., Pohl T.M., Portebeille D., Purnelle B., Rameyger U., Surzycki R., Thebaud P., Vandembol M., Vornueler F.J., Weidner S., Wells D.E., Wong K., Yeh K.-C., Batut J.;		
DR EMBL: AP002515; BAB97786.1; -;	RA Rameyger U., Surzycki R., Thebaud P., Vandembol M., Vornueler F.J., Weidner S., Wells D.E., Wong K., Yeh K.-C., Batut J.;		
DR EMBL: BX9272149; CAFL19108.1; -;	RA Vornueler F.J., Weidner S., Wells D.E., Wong K., Yeh K.-C., Batut J.;		
XN Complete proteome; Hypothetical protein.	RA "The composite genome of the legume symbiont <i>Sinorhizobium meliloti</i> strain 1021.";		
SQ SEQUENCE 279 AA; MW: 29006 MW; AA5BCD021149FD2E CRC64;	RA Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).		
Qy Query Match Score 50; DB 2; Length 279;	CC !-- SIMILARITY: Belongs to the ppIC/parrulin rotamase family.		
DB Best Local Similarity 44.2%; Pred. No. 1.1e+02;	CC DR EMBL: AL591791; CAC7205.1; -.		
DB Matches 12; Conservative 2; Mismatches 11; Indels 0; Gaps 0;	DR HSSP; P21202; 1MSY;		
Qy 1 MKRMKSLLAALTVALGAMLAAPVATA 25	DR GO; GO:0016853; Fis somerase activity; IEA.		
Db 1 MNRFPSALLAASVAGAAALAPVATA 25	DR GO; GO:0006457; F:prolyl-prolyl cis-trans isomerase activity; IEA.		
Q92KJ0 PRELIMINARY; PRT; 279 AA.	DR InterPro; IPR00297; Rotamase.		
RESULTS 31	DR Pfam; PF00639; Rotamase; 1.		
CAFI9108 ID CAFI9108 PRELIMINARY; PRT; 279 AA.	DR PROSITE; PS50158; PPIC_PPASE_2; 1.		
AC CAFI9108 PRELIMINARY; PRT; 279 AA.	DR KW Complete proteome; Isomerase; Rotamase.		
DT 02-MAR-2004 (TREMBLrel. 27, Created)	SQ SEQUENCE 284 AA; 31460 MW; 700277987D225C53 CRC64;		
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)	Query Match Score 50; DB 2; Length 284;		
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)	Best Local Similarity 60.0%; Pred. No. 1.1e+02;		
DE Conserved secreted protein.	Matches 15; Conservative 2; Mismatches 6; Indels 2; Gaps 1;		
GN CG471.	Qy 1 MKRMKSLLAALTVALGAMLAAPVATA 25		
OS Corynebacterium glutamicum (Brevibacterium flavum).	Db 1 MSYKTIKAAALV-AMIAVGVARA 23		
OC Bacteria; Actinobacteria; Actinomycetales;	RESULTS 33		
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.			
OX NCBI_TaxID=1718;			
RN SEQUENCE FROM N.A. / DSM 20300 / NCIB 10025;			
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;			
RA Kalinowski J., Bathé B., Bartels D., Bischoff N., Bott M., Gaiglak L.,			
RA Burkhardt A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,			
RA McHardy A.-C., Meyer F., Moekel B., Pfefferle W., Puehler A.,			
RA Rey D.A., Rueckert C., Rupp O., Sähm H., Wendisch V.F., Wiegraebe I.,			
RA Tauch A.;			
RA "The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins";			
RR J. Biotechnol. 104:5-25(2003).			
DR EMBL: BX9272149; CAFL19108.1; AA5BCD021149FD2E CRC64;			
SEQUENCE 279 AA; MW: 29006 MW; AA5BCD021149FD2E CRC64;			

Qy	2 KENKSLAAALTIVAGAMLAAPVATA 25	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
Db	: : : : :	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
	21 RMMKRPLVAMLTAVMLACPLALA 44	DE	Putative small secreted protein.
		GN	OrderedLocusNames=SC01800; ORFNAMES=SC15.08c;
		OS	Streptomyces coelicolor.
		OC	Bacteria; Actinobacteria; Actinomycetales; Streptomyces;
		OC	Streptomycineae; Streptomyctaceae; Streptomyces.
		RN	[1] NCBITaxID=1502;
		RP	"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."
		RT	Nature 417:141-147 (2002).
		RL	DR
		EMBL	AL391101; CAB45232; -.
		DR	PIR: T36861; T36861.
		DR	InterPro: IPR005528; DUF320..
		PFam	PF03777; DUF220; 1.
		KW	Complete proteome.
		SQ	SEQUENCE 82 AA: 7760 MW: 040056985A7E07C CRC64;
		Query Match	Best Local Similarity 43.4%; Score 49; DB 2; Length 82;
		Best Local Similarity 60.9%; Pred. No. 95; DB 2; Length 185;	Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
		Best Local Similarity 60.9%; Pred. No. 95; DB 2; Length 185;	Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
		Qy	3 RMKSLAAALTIVAGAMLAAPVATA 25
		Db	12 RMSTLAAALT-ACLTAPGATA 33
		RESULT 37	RESULT 38
Qy	2 KENKSLAAALTIVAGAMLAAPVATA 25	ID	AAS05087
Db	: : : : :	AC	AAS05087;
	21 RMMKRPLVAMLTAVMLACPLALA 44	DT	02-MAR-2004 (TREMBLrel. 27, Created)
		DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
		DE	Hypothetical protein.
		OS	Mycobacterium paratuberculosis.
		OC	Bacteria; Actinobacteria; Actinomycetales;
		OC	Corynebacterineae; Mycobacterium; Mycobacterium;
		OC	Mycobacterium avium complex (MAC).
		OX	NCBI_TaxID=1770;
		RN	SEQUENCE FROM N.A.
		RC	Li L., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.; Submitted (SPP-2003) to the EMBL/GenBank/DBU databases.
		RL	DR
		EMBL	AE017237; AAS05087.1; -.
		KW	Complete proteome; Hypothetical protein.
		SQ	SEQUENCE 185 AA; 19136 MW; 3E4D53FB00851873 CRC64;
		Query Match	Best Local Similarity 43.8%; Score 49.5; DB 2; Length 185;
		Best Local Similarity 60.9%; Pred. No. 95; DB 2; Length 185;	Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
		Qy	3 RMKSLAAALTIVAGAMLAAPVATA 25
		Db	12 RMSTLAAALT-ACLTAPGATA 33
		RESULT 37	RESULT 38
Qy	2 KENKSLAAALTIVAGAMLAAPVATA 25	ID	AAS05087
Db	: : : : :	AC	AAS05087;
	21 RMMKRPLVAMLTAVMLACPLALA 44	DT	02-MAR-2004 (TREMBLrel. 27, Created)
		DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)
		DE	Hypothetical protein.
		OS	Mycobacterium paratuberculosis.
		OC	Bacteria; Actinobacteria; Actinomycetales;
		OC	Corynebacterineae; Mycobacterium; Mycobacterium.
		OX	NCBI_TaxID=1770;
		RN	SEQUENCE FROM N.A.
		RC	Li L., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.; Submitted (SPP-2003) to the EMBL/GenBank/DBU databases.
		RL	DR
		EMBL	AE017237; AAS05087.1; -.
		KW	Hypothetical protein.
		SQ	SEQUENCE 185 AA; 19136 MW; 3E4D53FB00851873 CRC64;
		Query Match	Best Local Similarity 43.8%; Score 49.5; DB 2; Length 185;
		Best Local Similarity 60.9%; Pred. No. 95; DB 2; Length 185;	Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
		Qy	3 RMKSLAAALTIVAGAMLAAPVATA 25
		Db	12 RMSTLAAALT-ACLTAPGATA 33
		RESULT 39	RESULT 39
Qy	2 KENKSLAAALTIVAGAMLAAPVATA 25	ID	Q9X922
Db	: : : : :	AC	Q9X922;
	21 RMMKRPLVAMLTAVMLACPLALA 44	DT	01-NOV-1999 (TREMBLrel. 12, Created)
		DE	
		GN	
		OS	
		OC	
		OC	
		RN	[1] NCBITaxID=1502;
		RP	"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."
		RT	Nature 417:141-147 (2002).
		RL	DR
		EMBL	AL391101; CAB45232; -.
		DR	PIR: T36861; T36861.
		DR	InterPro: IPR005528; DUF320..
		PFam	PF03777; DUF220; 1.
		KW	"Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris."
		RN	Biotechnol. 22:155-161 (2004).
		EMBL	BX572607; CAE9821.1; -.
		DR	InterPro: IPR001568; RNase T2.
		DR	PFam: PF00445; Ribonuclease T2; 1.
		DR	PROSITE: PS00530; RNASE T2_1; 1.
		KW	Complete proteome; Signal.
		FT	SIGNAL 1
		SEQUENCE	SEQUENCE 231 AA; 26028 MW; BC5AE77C4AA624 CRC64;
		Query Match	Score 49; DB 2; Length 231;

Best Local Similarity 45.8%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 0;
Gaps 0;

QY :| :| | | | | :| | |
2 KRMKSLAAALTVAGAMLAAPVATA 25
Db 6 RRRRLIAACAVVGALFTSVAEA 29

Search completed: December 1, 2004, 11:50:12
Job time : 192 secs

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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:41:50 ; Search time 37 Seconds
(without alignments)
44.809 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113

Sequence: 1 MKENKSLAAALTYAGANLAAPVATA 25

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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 2: /egn2_6/pctodata/1/iaa/5B_COMBO.pep:
 3: /egn2_6/pctodata/1/iaa/6A_COMBO.pep:
 4: /egn2_6/pctodata/1/iaa/6B_COMBO.pep:
 5: /egn2_6/pctodata/1/iaa/PCTUS_COMBO.pep:
 6: /egn2_6/pctodata/1/iaa/backfiles.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	51	45.1	107	3	US-08-818-112-83		Sequence 83, Appl
2	51	45.1	107	3	US-08-818-111-04		Sequence 84, Appl
3	51	45.1	107	3	US-09-056-556-03		Sequence 83, Appl
4	51	45.1	107	4	US-09-072-596-84		Sequence 84, Appl
5	51	45.1	107	4	US-03-072-596-83		Sequence 83, Appl
6	51	45.1	168	3	US-08-818-112-100		Sequence 100, App
7	51	45.1	168	3	US-08-818-111-15		Sequence 95, Appl
8	51	45.1	168	3	US-09-056-556-100		Sequence 100, App
9	51	45.1	168	4	US-09-072-596-35		Sequence 95, Appl
10	51	45.1	168	4	US-09-072-967-100		Sequence 100, App
11	51	45.1	187	3	US-08-818-112-63		Sequence 63, Appl
12	51	45.1	187	3	US-08-818-111-64		Sequence 64, Appl
13	51	45.1	187	3	US-09-056-556-63		Sequence 63, Appl
14	51	45.1	187	4	US-09-072-596-64		Sequence 64, Appl
15	51	45.1	187	4	US-09-072-967-63		Sequence 63, Appl
16	46	40.7	470	4	US-09-328-152-397		Sequence 5397, Appl
17	45	39.8	229	4	US-09-270-167-40998		Sequence 40398, A
18	45	39.8	229	4	US-09-270-167-56214		Sequence 56214, A
19	45	39.8	322	4	US-09-489-139A-9408		Sequence 9408, Ap
20	45	39.8	563	3	US-08-362-125-12		Sequence 12, Appl
21	45	39.8	659	3	US-08-894-819B-1		Sequence 1, Appl
22	45	39.8	659	3	US-09-445-472-12		Sequence 12, Appl
23	45	39.8	659	4	US-10-090-624-12		Sequence 12, Appl
24	45	39.8	1264	4	US-09-252-991A-30264		Sequence 30264, A
25	44.5	39.4	191	4	US-09-270-167-5622		Sequence 3522, A
26	44.5	39.4	303	3	US-09-270-167-56239		Sequence 50339, A
27	44.5	39.4	303	3	US-09-159-106-13		Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-818-112-83
; Sequence 83, Application US/08818112
; Patent No. 6290939
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Speiky, Yassir A. W.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Roughton, Raymond C.
; APPLICANT: Dillon, C.
; APPLICANT: Vediwick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSTICS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-1900
; TELEFAX: (206) 632-6031
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-818-112-83
; Query Match Score 51, DB 3, Length 107;
; Best Local Similarity 60.0%; Pred. No. 1.7;
; Matches 12; Conservative 3; Mismatches 5; Indels 0;
; Gaps 0;

STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/056,556
 FILING DATE: 07-APR-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.457
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-056-556-83

Query Match 45.1% Score 51; DB 3; Length 107;
 Best Local Similarity 60.0%; Pred. No. 1.7; Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 4
 US-09-072-596-84

Query Match 45.1% Score 51; DB 3; Length 107;
 Best Local Similarity 60.0%; Pred. No. 1.7; Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Query Match 45.1% Score 51; DB 3; Length 107;
 Best Local Similarity 60.0%; Pred. No. 1.7; Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 4

US-09-072-596-84

Sequence 84, Application US/08181111
 Patent No. 6338852

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonia
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,111
 FILING DATE: 13-MAR-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-818-111-84

Query Match 45.1% Score 51; DB 3; Length 107;
 Best Local Similarity 60.0%; Pred. No. 1.7; Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 3

US-09-056-556-83

Sequence 83, Application US/09056556
 Patent No. 6354456

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND TREATMENT OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 241
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle

STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-072-967-84

Query Match Best Local Similarity Score DB Length
 Matches 12; Conservative 60.0%; 51; 4; 107;
 Qy 1 MGRMKSLAAALTVGAMLA 20
 Db 10 MGRVKSIAAGLTAAAIGAA 29

RESULT 5
 US-09-072-967-83
 Sequence No. Application US/09072967
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedyick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TUBERCULOSIS
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,112
 FILING DATE: 13-MAR-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121-411C6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-818-112-100

Query Match Best Local Similarity Score DB Length
 Matches 12; Conservative 60.0%; 51; 3; 168;
 Qy 1 MGRMKSLAAALTVGAMLA 20
 Db 1 MGRVKSIAAGLTAAAIGAA 29

RESULT 7
 US-08-818-111-95
 Sequence 95, Application US/08818111
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedyick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:

Query Match Best Local Similarity Score DB Length
 Matches 12; Conservative 60.0%; 51; 4; 107;
 Qy 1 MGRMKSLAAALTVGAMLA 20
 Db 1 MGRVKSIAAGLTAAAIGAA 29

ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/818,111
 FILING DATE: 13-MAR-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,352
 REFERENCE/DOCKET NUMBER: 210121.417C6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 95:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-818-111-95

Query Match 45.1%; Score 51; DB 3; Length 168;
 Best Local Similarity 60.0%; Pred. No. 2.9;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTVGAMLLA 20
 Db 1 MRKVKSIAAGLTAAGAIGAA 20

RESULT 8
 US-09-056-556-100
 Sequence 100, Application US/09056556
 Patent No. 6350456
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A. W.
 APPLICANT: Dillon, Devin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
 TREATMENT OF SEVERAL DISEASES
 NUMBER OF SEQUENCES: 241
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 95:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-072-556-95

Query Match 45.1%; Score 51; DB 4; Length 168;
 Best Local Similarity 60.0%; Pred. No. 2.9;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTVGAMLLA 20
 Db 1 MRKVKSIAAGLTAAGAIGAA 20

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.457
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 100:

```

US-09-072-967-100
; Sequence 100, Application US/09072967
; Patent No. 6592877

; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Veditck, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.

; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mai, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-072-967-100

Query Match          45.1%; Score 51; DB 4; Length 168;
Best Local Similarity 60.0%; Pred. NO. 2.9; Mismatches 5; Indels 0
Matches 12; Conservative 3; Nucleotides: 153

Qy      1 MGRKNSLAAALTAGAMLLA 20
Db      1 MRYKNSIAGLTAAGAAGGA 20

RESULT 11
US-08-818-112-63
; Sequence 63, Application US/0881812
; Patent No. 6290069

; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Veditck, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERRY LLP

```

STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,112
 FILING DATE: 13-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 ID NO: 63:
 SEQUENCE INFORMATION FOR SEQ ID NO:
 LENGTH: 187 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 -818-112-63

TRY Match 45.1%; Score 51; DB 3; Len 5;
 TRY Local Similarity 60.0%; Pred. No. 3.2; Mismatches 5;
 matches 12; Conservative 3; Mismatches 5;

1 MKRMRKSIAAAATVAGAMLA 20
 || :|| :|| :|| :|| :||
 20 MKMVKSTAAGTAAAIGAA 39

12-
 -818-111-64
 Sequence 64, Application US/08818111
 ent No. 6338852
 INTERNAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonia
 APPLICANT: Houghton, Raymond S.
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DI
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEDB and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,111
 FILING DATE: 13-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C6
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 622-6011
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-818-111-64

Query Match Score 51; DB 3; Length 187;
 Best Local Similarity 60.0%; Pred. No. 3.2%;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAAGMLAA 20
 Db 20 MKMVKSIAAGTAAAGAA 39

RESULT 13
 US-09-056-556-63
 Sequence 63, Application US/09056556
 ; Patent No. 6350456
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Sheiky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND TREATMENT OF SEQUENCES: 241
 NUMBER OF SEQUENCES: 241
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-072,596-64

Query Match Score 51; DB 4; Length 187;
 Best Local Similarity 60.0%; Pred. No. 3.2%;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAAGMLAA 20
 Db 20 MKMVKSIAAGTAAAGAA 39

RESULT 15
 US-09-072-967-63
 Sequence 63, Application US/09072967
 ; Patent No. 659287
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Sheiky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campor-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedula, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle

Query Match Score 51; DB 3; Length 187;
 Best Local Similarity 60.0%; Pred. No. 3.2%;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVAAGMLAA 20
 Db 20 MKMVKSIAAGTAAAGAA 39

RESULT 14
 US-09-072-596-64
 Sequence 64, Application US/09072596
 ; Patent No. 6458366

STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,967
 FILING DATE: 05-MAY-1998
 CLASSIFICATION INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31-392
 REFERENCE/DOCKET NUMBER: 210121.411C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 US-09-072-967-63

Query Match Score 51; DB 4; Length 187;
 Best Local Similarity 60.0%; Pred. No. 3.2%;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRKKSLAAALTVAGAMIAA 20
 Db 20 MRMVKSIAAGLTAAAIGAA 39

RESULT 16
 US-09-328-352-5397
 Sequence 5397, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: GTIC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 5397
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-5397

Query Match Score 46; DB 4; Length 470;
 Best Local Similarity 43.5%; Pred. No. 51;
 Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 3 RMKSLAAALTVAGAMIAAPVATA 25
 4 RMKRMALMSLTGALLGGTAWA 27

RESULT 17
 US-09-270-167-40998
 Sequence 40998, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17

RESULT 18
 US-09-270-767-56214
 Sequence 56214, Application US/09270767
 Patient No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7336-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SEQ ID NO 56214
 LENGTH: 229
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-56214

Query Match Score 45; DB 4; Length 229;
 Best Local Similarity 42.9%; Pred. No. 32%;
 Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 4 MKSLAAALTVAGAMIAAPVAT 24
 5 VKSMAKKISAGDQVLAPVVT 227

RESULT 19
 US-09-489-039A-9408
 Sequence 9408, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 FILE REFERENCE: 2709-2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 9408
 LENGTH: 322
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-9408

Query Match Score 45; DB 4; Length 322;
 Best Local Similarity 50.0%; Pred. No. 47%;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MKRKKSLAAALTVAGAMIAA 20
 Db 25 MRKKYKLSTLIVAAVALIAA 44

RESULT 20
US-08-362-525-12
Sequence 12, Application US/08362525
Patent No. 602910
GENERAL INFORMATION:
APPLICANT: KLIS, FRANCISCUS M.
APPLICANT: SCHREUDER, MARTEL P.
APPLICANT: TOSCHA, HOLGER Y.
APPLICANT: VERRIPS, CORNELIS T.
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE
TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-1918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,525
FILING DATE: 04-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 922 02080.5
FILING DATE: 08-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 922 03899.7
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/01763
FILING DATE: 07-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 213289/T7420 (V)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (02) 861-3000
TELEFAX: (02) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 563 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-525-12

APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894, 818B
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAKAKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3548
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-818B-1

Query Match 39.8%; Score 45; DB 3; Length 659;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

Qy 1 MKRMRKSLAALT---VAGAMLLAAPV 22
Db 1 MKRLGAVVLVNLGLAGTALAAAPV 26

RESULT 22
US-08-445-472-12
Sequence 12, Application US/09445472
Patent No. 6358726
GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: US/09/445, 472
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151369/1997
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 659
TYPE: PRT
ORGANISM: Thermococcus celer

RESULT 21
US-08-894-818B-1
Sequence 1, Application US/08894818B
Patent No. 6261822
GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MITTA, Masanori
APPLICANT: ASADA, Kiyozo

US-09-445-472-12

Query Match 39.8%; Score 45; DB 3; Length 659;
Best Local Similarity 46.2%; Pred. No. 1.1e+02; Indels 4; Gaps 1;
Matches 12; Conservative 4; Mismatches 6;

RESULT 23
US-10-090-624-12
; Sequence 12, Application US/10090624
; Patent No. 6783970
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikuoshin.
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; CURRENT APPLICATION NUMBER: US/10/090,624
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 99/1445,472
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 12
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Thermococcus celer

US-10-090-624-12

Query Match 39.8%; Score 45; DB 4; Length 659;
Best Local Similarity 46.2%; Pred. No. 1.1e+02; Indels 6; Gaps 1;
Matches 12; Conservative 4; Mismatches 6;

RESULT 24
US -09-252-991A-30264
; Sequence 30264, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenstein et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSBUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 1264
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30264

Query Match 39.8%; Score 45; DB 4; Length 1264;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 12; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

RESULT 25
US-09-270-767-35622
; Sequence 35622, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SEQ ID NO 35622
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-09-270-767-35622

Query Match 39.4%; Score 44.5; DB 4; Length 191;
Best Local Similarity 70.0%; Pred. No. 31; Mismatches 5; Indels 1; Gaps .

RESULT 26
US-09-270-767-50839
; Sequence 50839, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50839
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-09-270-767-50839

Query Match 39.4%; Score 44.5; DB 4; Length 191;
Best Local Similarity 70.0%; Pred. No. 31; Mismatches 5; Indels 1; Gaps .

RESULT 27
US-09-159-106-13
; Sequence 13, Application US/09159106
; Patent No. 6288509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diaz, Ivan
; APPLICANT: Halkier, Torben
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 4633-200-US
; CURRENT APPLICATION NUMBER: US/09/159,106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/956

Query Match 39.8%; Score 45; DB 4; Length 1264;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 12; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

RESULT 28
US-09-251-991A-30264
; Sequence 30264, Application US/09251991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenstein
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSBUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 1264
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-251-991A-30264

```

; PRIORITY APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 13
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-13

Query Match   Score 44.5%; DB 3; Length 303;
Best Local Similarity 56.5%; Pred. No. 53;
Matches 13; Conservative 2; Mismatches 7;
Indels 1; Gaps 1;
Qy  2 KRMKS-LAALTVAGAMILAAPVA 23
Db  24 RRLASALVALTAALAAALATVA 46

RESULT 28
US-09-159-106-11

Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Ferrer, Pau
; APPLICANT: Diers, Ivan
; APPLICANT: Halkier, Torben
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 469-204-US
; CURRENT APPLICATION NUMBER: US/09/159,106
; CURRENT FILING DATE: 1998-09-03
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-14
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 11
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

Query Match   Score 39.4%; DB 3; Length 435;
Best Local Similarity 56.5%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 7;
Indels 1; Gaps 1;
Qy  2 KRMKS-LAALTVAGAMILAAPVA 23
Db  24 RRLASALVALTAALAAALATVA 46

RESULT 29
US-09-154-750A-83

Sequence 83, Application US/09154750A
; Patent No. 64315640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; FILE REFERENCE: 1107-75157
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIORITY APPLICATION NUMBER: 1997-09-14
; PRIORITY NUMBER: 09154750A
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4830

Query Match   Score 44%; DB 4; Length 284;

```

Best Local Similarity 55.0%; Pred. No. 58;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MGRMKSLAAALTVAGMLAAPVA 20
Db 3 ICKWGLGLALATVAGLAAA 22

RESULT 32
US-09-252-991A-25482
; Sequence 25482, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25482
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25482

Query Match 38.9%; Score 44; DB 4; Length 415;
Best Local Similarity 43.5%; Pred. No. 89;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MGRMKSLAAALTVAGMLAAPVA 23
Db 203 LHRUGPVAAAPASAAGQSLLAAPVA 225

RESULT 33
US-09-252-991A-27669
; Sequence 27669, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27669
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27669

Query Match 38.9%; Score 44; DB 4; Length 681;
Best Local Similarity 43.5%; Pred. No. 1.5e+02;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MGRMKSLAAALTVAGMLAAPVA 23
Db 264 LTRVGSLLASVRLGALLAVGTA 286

RESULT 36
US-09-105-90-22
; Sequence 22, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; NUMBER OF SEQUENCES: 66
; TITLE OF INVENTION: and Genes
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA

RESULT 34
US-09-252-991A-25257
; Sequence 25257, Application US/09252991A

COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,390
 FILING DATE: Filed herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/050,675
 FILING DATE: 25-JUN-97
 ATTORNEY/AGENT INFORMATION:
 NAME: Petithory, Joanne R.
 REGISTRATION NUMBER: P42,995
 REFERENCE/DOCKET NUMBER: 2000-0455-30
 TELECOMMUNICATION:
 TELEPHONE: 650-324-0980
 TELEX: 650-324-0960
 TELEX:
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-09-105,390-22

Query Match Best Local Similarity 38.5%; Score 43.5; DB 3; Length 30;
 Matches 11; Conservative 6; Indels 3; Gaps 1;

Qy 1 MKRMKSLAAALTVN--GAMLAAPVATA 25
 Db 1 MARROGVASMLTIALIIGFASAPTSCA 28

RESULT 37
 Patent No. 5217891-4
 ;APPLICANT: BRAKE, ANTHONY J.; VAN DEN BERG, JOHAN A.
 ;TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUTVEROMYCES
 ;A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
 ;POLYPEPTIDES
 ;NUMBER OF SEQUENCES: 23
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/507,398
 FILING DATE: 09-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 78,551
 FILING DATE: 28-JUL-1987
 SEQ ID NO: 4;
 LENGTH: 187

Query Match Best Local Similarity 38.1%; Score 43; DB 6; Length 187;
 Matches 10; Conservative 5; Indels 9; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLAAPVAT 24
 Db 1 MKFESTILAASTALISVNAAPVST 24

RESULT 38
 US-09-270-767-32610
 ;Sequence 32610, Application US/09270767
 ;Patent No. 6703491
 ;GENERAL INFORMATION:

/* APPLICANT: Homburger et al.
 /* TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 /* FILE REFERENCE: File Reference: 7326-094
 /* CURRENT APPLICATION NUMBER: US/09/270,767
 /* NUMBER OF SEQ ID NOS: 62517
 /* CURRENT FILING DATE: 1999-03-17
 /* SEQ ID NO: 32610
 /* SOFTWARE: PatentIn Ver. 2.0
 /* LENGTH: 190
 /* TYPE: PRT
 /* ORGANISM: *Drosophila melanogaster*
 /* US-09-270-767-32610

RESULT 39
 US - 09 - 270 - 767 - 47827
 ; Sequence 47827, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; SEQ ID NO: 47827
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 ; US-09-270-767-47827

Query Match Best Local Similarity 38.1%; Score 43; DB 4; Length 190;
 Matches 9; Conservative 4; Indels 8; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLAAP 21
 :||: :|||: :|||:
 Db 7 IKRIAEIAVAYAKAGAHIVAP 27

RESULT 40
 5217891-15
 ;Patent No. 5217891
 ;APPLICANT: BRAKE, ANTHONY J.; VAN DEN BERG, JOHAN A.
 ;TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUTVEROMYCES
 ;A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
 ;POLYPEPTIDES
 ;NUMBER OF SEQUENCES: 23
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/507,398
 FILING DATE: 09-APR-1990
 ;APPLICATION NUMBER: 78,551
 FILING DATE: 28-JUL-1987
 ;SEQ ID NO: 15;
 LENGTH: 458

Query Match Best Local Similarity 38.1%; Score 43; DB 6; Length 458;
 Matches 10; Conservative 5; Indels 9; Gaps 0;

Qy 1 MKRMKSLAAALTVAGAMLAAPVAT 24

Db 1 MKFSTILAASTALISYMAAPVST 24

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Job time : 39 secs

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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:50:21 ; Search time 145 Seconds

(without alignments)
61.487 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113

Sequence: 1 MKRMKSLAAALTVAGMLAAPVATA 25

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SUMMARIES

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SUMMARIES

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1 113 100.0 25 14 US-10-112-488-2 Sequence 2, Appli

2 113 100.0 25 16 US-10-673-860-3 Sequence 3, Appli

3 57 50.4 395 9 US-09-738-626-664 Sequence 6,4, Ap

4 55 48.7 526 16 US-10-437-963-190930 Sequence 190930,

5 51.5 45.6 87 14 US-10-156-761-12894 Sequence 12894, A

6 51 45.1 104 9 US-09-738-226-4865 Sequence 4885, Ap

7 51 45.1 107 14 US-10-193-002-84 Sequence 8,1, Appli

8 51 45.1 107 14 US-10-084-843-83 Sequence 83, Appli

9 51 45.1 168 14 US-10-080-170-334 Sequence 54, Appli

10 51 45.1 168 14 US-10-193-002-95 Sequence 54, Appli

11 51 45.1 168 14 US-10-084-843-100 Sequence 100, Appli

12 51 45.1 168 16 US-10-080-170-534 Sequence 534, Appli

13 51 45.1 168 17 US-10-468-356-534 Sequence 534, Appli

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RESULT 2
US-10-673-860-3
Sequence 3, Application US/10673860
Publication No. US2004126847A1
GENERAL INFORMATION:
APPLICANT: Ajinomoto Co., Inc.
TITLE OF INVENTION: A method of secreting and producing proteins
FILE REFERENCE: Y1J0182
CURRENT APPLICATION NUMBER: US/10/673,860
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: JP 2001-98808
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 3
LENGTH: 25
TYPE: PRF
ORGANISM: Corynebacterium ammoniagenes
US-10-673-860-3

Query Match 100.0%; Score 113; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Qy 1 MKRMSLAAALTVAGAMLAAPVATA 25
Db 1 MKRMSLAAALTVAGAMLAAPVATA 25

RESULT 3
US-09-738-626-6644
Sequence 644, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, MIKIRO
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 0/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 0/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO: 6644
TYPE: PRF
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6644

Query Match 50.4%; Score 57; DB 9; Length 395;
Best Local Similarity 66.7%; Pred. No. 4.6; Indels 3; Gaps 0;
Matches 12; Conservative 3; Mismatches 3;

Qy 2 XRMKSLAAALTVAGAMLA 19
Db 13 XRLKPLAAAVALAVAGVILLA 30

RESULT 2
US-10-437-963-190930
Sequence 190930, Application US/10437963
Publication No. US20040123333A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbatzuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO: 190930
LENGTH: 526
TYPE: PRF
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(526)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_87298C.1.pep
US-10-437-963-190930

Query Match 48.7%; Score 55; DB 16; Length 526;
Best Local Similarity 54.2%; Pred. No. 12; Mismatches 7; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 KERMKSLLAAALTVAGMLAAPVATA 25
Db 6 RRRRRRAAVVAVVALLASARTA 29

RESULT 5
US-10-156-761-12894
Sequence 12894, Application US/10156761
Publication No. US20030115018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADOTSU
APPLICANT: SAWAKI, YOSHIOUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204389
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO: 12894
LENGTH: 87
TYPE: PRF
ORGANISM: Streptomyces avermitilis
US-10-156-761-12894

Qy 4 MKMSLAAALTVAGAM-LAAPVATA 25
Db 1 MMSLKAAVAVGAVAVGAVAVA 23

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 83:
 US-10-084-843-83

Query Match 45.1%; Score 51; DB 14; Length 107;
 Best Local Similarity 60.0%; Pred. No. 8.2;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSTAAALTYAGMLAA 20
 Db 10 MKMVKSIAAGTAAAAGAA 29

RESULT 9
 US-10-080-170-534
 Sequence 534, Application US/10080170
 Publication No. US2003012960A1
 GENERAL INFORMATION:
 APPLICANT: COLE, S. T.
 TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TREATMENT OF MYCOBACTERIOSSES
 FILE REFERENCE: 03495.0218
 CURRENT FILING DATE: 2002-06-10
 PRIOR APPLICATION NUMBER: 60/270,123
 PRIOR FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 652
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 534
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Mycobacterium tuberculosis

Query Match 45.1%; Score 51; DB 14; Length 107;
 Best Local Similarity 60.0%; Pred. No. 14;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSTAAALTYAGMLAA 20
 Db 10 MKMVKSIAAGTAAAAGAA 29

RESULT 10
 US-10-193-002-95
 Sequence 95, Application US/10193002
 NUMBER OF SEQ ID NOS: 356
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 ADDRESS: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 ZIP: 98104-7092
 COUNTRY: USA

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington

Query Match 45.1%; Score 51; DB 14; Length 168;
 Best Local Similarity 60.0%; Pred. No. 14;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSTAAALTYAGMLAA 20
 Db 10 MKMVKSIAAGTAAAAGAA 29

RESULT 11
 US-10-084-843-100
 Sequence 100, Application US/10084843
 Publication No. US20030143243A1
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 ADDRESS: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 ZIP: 98104-7092
 COUNTRY: USA

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 ZIP: 98104-7092
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-10-084, 843
 FILING DATE: 25-Feb-2002
 CLASSIFICATION: <Unknown>

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-10-084, 843
 FILING DATE: 25-Feb-2002
 CLASSIFICATION: <Unknown>

```

APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-084-843-100

Query Match 45.1%; Score 51; DB 14; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 534
Length: 168
Type: PRT
Organism: Mycobacterium tuberculosis
US-10-468-356-534

Query Match 45.1%; Score 51; DB 17; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 534
Length: 168
Type: PRT
Organism: Mycobacterium tuberculosis
US-10-468-356-534

Query Match 45.1%; Score 51; DB 17; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 534
Length: 168
Type: PRT
Organism: Mycobacterium tuberculosis
US-10-468-356-534

RESULT 14
US-10-193-002-64
Sequence 64, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skelly, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedrick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193_002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILE REFERENCE: 0349-00218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2000-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 534
Length: 168
Type: PRT
Organism: Mycobacterium tuberculosis
US-10-080-170-534

RESULT 12
Sequence 534, Application US/10080170
Publication No. US20040121322A9
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSIS
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSIS
FILE REFERENCE: 0349-00218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2000-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 534
Length: 168
Type: PRT
Organism: Mycobacterium tuberculosis
US-10-080-170-534

Query Match 45.1%; Score 51; DB 16; Length 168;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 534
Length: 168
Type: PRT
Organism: Mycobacterium tuberculosis
US-10-468-356-534

Query Match 45.1%; Score 51; DB 14; Length 187;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 534
Length: 168
Type: PRT
Organism: Mycobacterium tuberculosis
US-10-193-002-64

```

Qy 1 MGRMKSLAAALTVAGMLAA 20 ;
Db 20 MKMVKSLAAAGLTTAAAGAA 39 ;

RESULT 15
US-10-084-843-63 ; Sequence 63, Application US/10084843
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; Skeiky, Yasir A.W.
; Dillon, Davin C.
; Campos-Neto, Antonio
; Houghton, Raymond
; Vedwick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 3 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6310 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084, 843
; FILING DATE: 25-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072, 967
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mai, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6030
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
; US-10-084-843-63

Qy 1 MGRMKSLAAALTVAGMLAA 20 ; Score 51; DB 14; Length 187;
Db 20 MKMVKSLAAAGLTTAAAGAA 39 ; Best Local Similarity 60.0%; Prd. No. 15; Mismatches 3; Indels 0; Gaps 0;

RESULT 16
US-09-864-408A-8468 ; Sequence 8468, Application US/09864408A
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.

Qy 1 MGRMKSLAAALTVAGMLAA 20 ; Score 50; DB 11; Length 56;
Db 20 MKMVKSLAAAGLTTAAAGAA 39 ; Best Local Similarity 50.0%; Prd. No. 5.6; Mismatches 9; Indels 0; Gaps 0;

RESULT 17
US-09-738-626-3942 ; Sequence 3942, Application US/09738626
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; MIZOGUCHI, HIROSHI
; ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; OCHIAI, KEIKO
; YOKOI, HARUHIKO
; TATEISHI, NAOKO
; SENOH, AKIHIRO
; IKEDA, MASATO
; OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIORITY APPLICATION NUMBER: JP 99/377484
; PRIORITY FILING DATE: 1999-12-16
; PRIORITY APPLICATION NUMBER: JP 00/159162
; PRIORITY FILING DATE: 2000-04-07
; PRIORITY APPLICATION NUMBER: JP 00/280988
; PRIORITY FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO: 3942
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-3942

RESULT 18
US-10-455-115-326373 ; Sequence 326373, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO: 326373
 LENGTH: 66
 TYPE: PRT
 ORGANISM: Zea mays
 OTHER INFORMATION: Clone ID: MRT4577_60722C.1.pep
 US-10-425-115-326373

Query Match Score 49; DB 17; Length 66;
 Best Local Similarity 45.8%; Pred. No. 9.5%;
 Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 RESULT 19

Qy 1 MKRMSLAAALTYAGAMLAAPYAT 24
 Db 1 MARTQSIVAVFVVVAPVLLIAPART 24

RESULT 19
 US-10-389-566-1646
 Sequence 1646, Application US/10389566
 Publication No. US20040025202A1
 GENERAL INFORMATION:
 APPLICANT: Monsanto Technology, LLC
 APPLICANT: Laurie, Cathy C
 TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 CURRENT APPLICATION NUMBER: US/10/389,566
 FILE REFERENCE: 38-77(52200)D
 CURRENT FILING DATE: 2003-03-31
 PRIOR APPLICATION NUMBER: US 60/365,301
 PRIOR FILING DATE: 2002-03-15
 PRIOR APPLICATION NUMBER: US 60/391,786
 PRIOR FILING DATE: 2002-06-25
 PRIOR APPLICATION NUMBER: US 60/392,018
 PRIOR FILING DATE: 2002-06-26
 NUMBER OF SEQ ID NOS: 2459
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 1646
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Thermosynechococcus elongatus
 US-10-389-566-1646

Query Match Score 48; DB 16; Length 254;
 Best Local Similarity 57.9%; Pred. No. 29%;
 Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 RESULT 20

Qy 7 LAAALTYAGAMLAAPYAT 25
 Db 33 VSAAPVGGNNVAADVGA 51

RESULT 20
 US-10-425-115-335695
 Sequence 335695, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28
 SEQ ID NO: 49108
 LENGTH: 255
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE: OTHER INFORMATION: Clone ID: 700048791_FLI.pep
 US-10-425-114-49108

Query Match Score: 42.5%; Best Local Similarity: 51.9%; Pred. No.: 60; Matches: 14; Conservative: 2; Mismatches: 9; Indels: 2; Gaps: 1;

Qy 1 MKRMKS--1AAALTYAGMMLAPVATA 25
 Db 42 LARSKSLHIVVALTPRANKATPIAGA 68

RESULT 23
 US-10-437-963-190010
 ; Sequence 190010, Application US/10437963
 ; Publication No. US20040123143A1

GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yinhua
 APPLICANT: Cao, Yongwei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 LENGTH: 500
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_86464C.1.pep
 US-10-437-963-190010

Query Match Score: 42.5%; Best Local Similarity: 68.8%; Pred. No.: 1.3e+02; Matches: 11; Conservative: 1; Mismatches: 4; Indels: 0; Gaps: 0;

Qy 10 ALTTAGMMLAPVATA 25
 Db 153 ALTTAGVLPIAVATA 168

RESULT 24
 US-10-282-122A-50795
 ; Sequence 50795, Application US/10282122A
 ; Publication No. US2004029129A1

GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hasselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282-122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/244,578
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 50795
 LENGTH: 998
 TYPE: PRT
 ORGANISM: Bordetella pertussis
 US-10-282-122A-50795

RESULT 25
 US-10-282-122A-66333
 ; Sequence 66333, Application US/10282122A
 ; Publication No. US2004029129A1

GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hasselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282-122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1.
 SEQ ID NO: 49262
 LENGTH: 409
 TYPE: PRT
 ORGANISM: Burkholderia fungorum
 US-10-283-122A-49262

Query Match 41.6%; Score 47; DB 15; Length 409;
 Best Local Similarity 61.1%; Pred. No. 1.e+02;
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RMKSLAAATVAGMLAA 20
 Db 14 RTRSLAAALSVASCMFA 31

RESULT 29
 US-10-213-181-14
 Sequence 14, Application US/10/13181
 Publication No. US20030054484A1
 GENERAL INFORMATION:
 APPLICANT: Fong, Sherman
 GODDARD, Audrey
 GODOWSKI, Paul
 GRIMALDI, Christopher
 HILLIAN, Kenneth
 TUMAS, Daniel
 WATANABE, Colin
 WOOD, William
 ZHANG, Zemin
 TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
 CURRENT FILING DATE: 2002-08-05
 PRIOR APPLICATION NUMBER: US/10/213,181
 FILE REFERENCE: P3133R1C7

PRIOR APPLICATION NUMBER: US 10/052,594
 PRIOR FILING DATE: 2002-01-18
 PRIOR APPLICATION NUMBER: PCT/US00/30073
 PRIOR APPLICATION NUMBER: US 60/177,118
 PRIOR FILING DATE: 2000-01-20
 NUMBER OF SEQ ID NOS: 24
 SEQ ID NO 14
 LENGTH: 58
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-213-181-14

Query Match 41.6%; Score 47; DB 14; Length 458;
 Best Local Similarity 59.1%; Pred. No. 1.e+02;
 Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 MKSLAAATVAGMLAA 25
 Db 1 MRGLAVLTVALLAPGAGA 22

RESULT 30
 US-10-212-912-14
 Sequence 14, Application US/10212912
 Publication No. US2003007737A1
 GENERAL INFORMATION:
 APPLICANT: Fong, Sherman
 GODDARD, Audrey
 GODOWSKI, Paul
 GRIMALDI, Christopher
 HILLIAN, Kenneth
 TUMAS, Daniel
 WATANABE, Colin
 WOOD, William
 ZHANG, Zemin
 TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
 CURRENT FILING DATE: 2002-08-05
 PRIOR APPLICATION NUMBER: US 10/052,594
 PRIOR FILING DATE: 2002-01-18
 PRIOR APPLICATION NUMBER: PCT/US00/30073
 PRIOR APPLICATION NUMBER: US 60/177,118
 PRIOR FILING DATE: 2000-01-20
 NUMBER OF SEQ ID NOS: 24

```

; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-044-14

Query Match Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 MKSLIAALTYAGMLAAPVATA 25
Db 1 MRGLAVLTVLVALTLLAAGAGA 22

RESULT 32
US-10-213-182-14
Sequence 14, Application US/10213182
Publication No. US20030087380A1
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
Diseases
FILE REFERENCE: P3133RIC3
CURRENT APPLICATION NUMBER: US/10/213.182
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/052,594
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/172,059
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 14
LENGTH: 458
TYPE: PRT
ORGANISM: Homo Sapien
US-10-213-182-14

Query Match Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 MKSLIAALTYAGMLAAPVATA 25
Db 1 MRGLAVLTVLVALTLLAAGAGA 22

RESULT 33
US-10-213-060A-14
Sequence 14, Application US/10213060A
Publication No. US2003010063A1
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
Diseases
FILE REFERENCE: P3133RIC5
CURRENT APPLICATION NUMBER: US/10/213.052
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/052,594
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/177,118
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 14
LENGTH: 458
TYPE: PRT
ORGANISM: Homo Sapien
US-10-213-060A-14

Query Match Score 47; DB 14; Length 458;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 MKSLIAALTYAGMLAAPVATA 25
Db 1 MRGLAVLTVLVALTLLAAGAGA 22

RESULT 35
US-10-273-517-4
Sequence 4, Application US/10273517
Publication No. US2003143588A1
GENERAL INFORMATION:

```

APPLICANT: THORNTON, Michael B.; DING, Li
 APPLICANT: ARIVZU, Chandra S.; YAO, Monique G.
 APPLICANT: TRIBOUTEY, Catherine M.; LAL, Preeti G.
 APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
 APPLICANT: RAMKUMAR, Jayalaxmi; LU, Yan
 APPLICANT: CHAWLA, Narinder K.
 TITLE OF INVENTION: PHOSPHODIESTERASES
 FILE REFERENCE: PI-0136 USA
 CURRENT APPLICATION NUMBER: US10/273,517
 CURRENT FILING DATE: 2000-10-18
 PRIOR APPLICATION NUMBER: 60/241,100
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 60/18,234
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US01/20140
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: 60/213,741
 PRIOR FILING DATE: 2000-06-22
 SOFTWARE: PERL Program
 SEQ ID NO: 4
 LENGTH: 489
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20030143588A1 6390038CD1
 US-10-273-517-4

Query Match 41.6%; Score 47; DB 14; Length 489;
 Best Local Similarity 59.1%; Prod. No. 1.7e+02;
 Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 MKSLAAALTAVAGMLAAPVATA 25
 Db 32 MRGLAVLTVALTLLAGAGA 53

RESULT 37
 US-10-425-115-213257
 ; Sequence 21:257, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yinhua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-(1)5322 B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; SEQ ID NO: 213257
 ; LENGTH: 85
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_126089C.1.pep
 US-10-425-115-213257

Query Match 41.2%; Score 46.5; DB 17; Length 85;
 Best Local Similarity 78.8%; Prod. No. 29;
 Matches 14; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 8 AAALTAVAGMLAAPVATA 25
 Db 34 ARAIGVA-AMLAAPAAQA 50

RESULT 38
 US-10-243-552-496
 ; Sequence 496, Application US/10243552
 ; Publication No. US20030224379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Weng, Gezhi
 ; APPLICANT: Ma, Yuning
 ; TITLE OF INVENTION: Novel Nucleic Acids and
 ; Polypeptides
 ; CURRENT APPLICATION NUMBER: US/10/243,552
 ; PRIORITY NUMBER: US 60/322,511
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR FILING DATE: 2001-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIORITY NUMBER: US 09/488,725
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIORITY NUMBER: US 09/552,317
 ; CURRENT FILING DATE: 2000-04-15
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; PRIORITY NUMBER: US 09/125
 ; CURRENT FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: US 09/491,404
 ; PRIORITY NUMBER: US 09-01-5
 ; PRIOR FILING DATE: 2000-01-5

RESULT 36
 US-10-311-104-4
 ; Sequence 4, Application US/10311104
 ; Publication No. US20040054138A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: THORNTON, Michael
 ; APPLICANT: DING, Li
 ; APPLICANT: ARIVZU Chandra S.
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: TRIBOUTEY, Catherine M.
 ; APPLICANT: LAL, Preeti G.
 ; APPLICANT: HAFALIA, April J. A.
 ; APPLICANT: BAUGHN, Mariah R.
 ; APPLICANT: RAMKUMAR, Jayalaxmi
 ; APPLICANT: LU, Yan
 ; APPLICANT: CHAWLA, Narinder K.
 ; TITLE OF INVENTION: PHOSPHODIESTERASES
 ; FILE REFERENCE: PI-0136 PCT
 ; CURRENT APPLICATION NUMBER: US10/311,104
 ; PRIOR APPLICATION NUMBER: PCT/US01/20140
 ; PRIOR APPLICATION NUMBER: 60/213,741
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 60/218,234
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/241,100
 ; PRIOR FILING DATE: 2000-10-16
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 4
 ; LENGTH: 489
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

```

; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: Pt_FL_genes version 5.0
; SEQ ID NO: 496
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-532-496

Query Match 41.2%; Score 46.5%; DB 14; Length 196;
Best Local Similarity 59.1%; Pred. No. 74;
Matches 13; Conservative 2; Mismatches 4; Indels 3; Gaps 1;
Qy 7 LAALTVACAML--AAPVATA 25
Db 21 LARALLIAAFLATLAFIATA 42

RESULT 39
US-10-156-761-14005
; Sequence 14005, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HONIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIOUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO: 14005
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14005

Query Match 40.7%; Score 46%; DB 14; Length 81;
Best Local Similarity 40.0%; Pred. No. 33;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
Qy 1 MRMKSLAAALTVAGAMLAAPVATA 25
Db 1 VRNLKKVAATVVAAGLVAGAGMA 25

RESULT 40
US-10-437-963-191208
; Sequence 191208, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:41:27 ; Search time 38 Seconds
 (without alignments)
 63.301 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113

Sequence: MCKRNSLAAALTVAAGMLAAPVATA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	46.9	133	2 E72763	immunoglobulin lambda-1 chain V region like APB0098 [imported] - Aeropyrum pernix (strain E72763)
2	53	46.9	507	2 T35677	C;Species: Aeropyrum pernix
3	52	46.0	141	1 JC1287	C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
4	51	45.1	168	2 G70587	C;Accession: E72763
5	50	44.2	125	2 H71723	A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
6	49	43.4	82	2 T36861	A;Status: Preliminary
7	49	43.4	313	2 F90884	A;Residues: 1-133 <RAW>
8	49	43.4	141	1 A85734	A;Cross-references: UNIPROT:Q9YQG03; DDBJ:AP000058; PIDN:BAA79007.1; PIDN:BA
9	49	43.4	313	2 B64896	A;Experimental source: strain K1
10	49	43.4	317	2 JC1439	C;Genetics:
11	48	42.5	106	2 G71078	A;Gene: APB0098
12	48	42.5	136	2 P95868	RESULT 2
13	48	42.5	533	2 A32529	probable hydrolase - Streptomyces coelicolor
14	48	42.5	559	2 A48296	C;Accession: T35677
15	48	42.5	1010	2 I40329	C;Species: Streptomyces coelicolor
16	48	42.5	1234	2 E83415	C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
17	47.5	42.0	98	2 E90629	R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
18	47.5	42.0	98	2 F85480	R;Submitted to the EMBL Data Library, November 1997
19	47.5	42.0	596	2 A46414	A;Reference number: Z221586
20	47.5	42.0	597	2 C87381	A;Accession: T35677
21	47	41.6	89	2 AG0016	A;Status: preliminary; translated from GB/EMBL/DDBJ
22	47	41.6	172	2 H87431	A;Molecule type: DNA
23	47	41.6	173	2 T44619	A;Residues: 1-507 <MUR>
24	47	41.6	206	2 T36643	A;Cross-references: UNIPROT:O50506; EMBL:AL009199; PIDN:CAA15789.1; GSPDB:GN00070; SCOEDB:SC7B7.09C
25	47	41.6	389	2 AH3003	A;Experimental source: strain A3 (2)
26	47	41.6	398	2 A99280	C;Genetics:
27	47	41.6	548	2 AG7357	A;Gene: SCOEDB:SC7B7.09C
28	47	41.6	719	2 T35189	Query Match Score 53; DB 2; Length 507;
29	46.5	41.2	502	2 A98151	Best Local Similarity 55.0%; Pred. No. 7.7; Mismatches 4; Indels 0; Gaps 0;

1 MCRMKSLAAALTIVAGAMLA 20

RESULT 3

Db :||: :||| | :||| :|||
 1 MRRMRSTRALTAATTAA 20

A;Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
 A;Reference number: A71630; MUID:903949; PMID:3823893
 A;Accession: H71723
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-15 <AND>
 A;Cross-references: UNIPROT:Q9ZB21; GB:AU235269; PIDN:g3860572; PIDN:CAA1460
 A;Experimental source: strain Madrid E
 C;Genetics:
 C;Superfamily: Escherichia coli ribosomal protein L12

Query Match 44.2%; Score 50; DB 2; Length 125;
 Best Local Similarity 60.0%; Pred. No. 6;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 6 SIAAALTIVAGMLAAPVATA 25
 Db 33 SAADAPITVASRGVAAFLAEA 52

RESULT 6

T36861
 Probable small secreted protein - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T36861
 R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A;Reference number: 221616
 A;Accession: T36861
 A;Status: Preliminary; translated from GB/EMBL/DDBU
 A;Molecule type: DNA
 A;Residues: 1-82 <SPE>
 A;Cross-references: UNIPROT:Q9X9Z2; EMBL:AU079332; PIDN:CA845292.1; GSPDB:GN00070; SCOBID
 C;Genetics:
 C;Experimental source: strain A3 (2)

Query Match 43.4%; Score 49; DB 2; Length 82;
 Best Local Similarity 44.0%; Pred. No. 5; 8;
 Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTIVAGMLAAPVATA 25
 Db 1 MONLKKAAAATVAGGLIAGAGMA 25

RESULT 7

F90884
 probable transport system permease protein ECs2046 [imported] - *Escherichia coli* (strain
 C;Species: *Escherichia coli*
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: F90884
 R;Hayashi, T.; Makino, K.; Ohnishi, N.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasavara, N.; Yasunaga, T.; Kuwahara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 A;Author: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: G70587
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-168 <COL>
 A;Cross-references: UNIPROT:Q05822; GB:Z95208; PIDN:CA804746
 A;Experimental source: strain H37Rv
 C;Genetics:
 A;Gene: Rv2346C

Query Match 45.1%; Score 51; DB 2; Length 168;
 Best Local Similarity 60.0%; Pred. No. 5; 6;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTIVAGMLAAPVATA 20
 Db 1 MRDYKSLAAGLTAAAGMA 20

RESULT 5

H71723
 ribosomal protein L7/L12 - *Rickettsia prowazekii*
 C;Species: *Rickettsia prowazekii*
 C;ID: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 C;Accession: H71723
 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.; Nature 396, 133-140, 1998
 A;Cross-references: UNIPROT:Q8X9W3; GB:BA000007; PIDN:BAB354469.1; PID:913361512; GSPDB:G
 A;Experimental source: strain O157:H7, substrate RIMD 0509952
 C;Genetics:
 C;Superfamily: spermidine/putrescine transport system permease protein poth
 Query Match 43.4%; Score 49; DB 2; Length 313;
 Best Local Similarity 47.6%; Pred. No. 18;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RMKSLAAALTYAGAMLAAPVA 23
Db 89 RLTMAVAVTASAILAFPNA 109

RESULT 8
A85734
A:probable transport system permease protein Z2277 [imported] - Escherichia coli (strain C)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85734
A:Residues: 1-313 <STO>
A:Cross-references: UNIPROT:Q8X9W3 ; GB:AE005174; NID:gi125152660; PIDN:ARG56333.1; GSPDB:G
A:Experimental source: strain O157:H7, substrate EDDL933
C:Genetics
A:Gene: Z2277
C:Superfamily: spermidine/putrescine transport system permease protein potH

Query Match Score 49; DB 2; Length 31;
Best Local Similarity 47.6%; Pred. No. 18;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RMKSLAAALTYAGAMLAAPVA 23
Db 89 RLTMAVAVTASAILAFPNA 109

RESULT 9
B64896
Probable membrane protein b1442 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: E64896
P:Blattner, F.R.; Plunkert III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; McClelland, M.; Rose, D.J.; Matz, B.; Shao, Y.
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:9278503
A:Status: nucleic acid sequence not shown; translation not shown
A:Keywords: spermidine/putrescine transport system permease protein potH
A:Molecule type: DNA
A:Residues: 1-313 <BLAT>
A:Cross-references: UNIPROT:P77156 ; GB:AE000241; GB:U00096; PIDN:AACT74524.
A:Experimental source: strain K-12, substrate MG1655
C:Superfamily: spermidine/putrescine transport system permease protein potH
C:Keywords: inner membrane; transmembrane protein

F:27-43 /Domain: transmembrane #status predicted <TM1>
F:90-106 /Domain: transmembrane #status predicted <TM2>
F:122-138 /Domain: transmembrane #status predicted <TM3>
F:188-204 /Domain: transmembrane #status predicted <TM4>
F:232-248 /Domain: transmembrane #status predicted <TM5>
F:288-304 /Domain: transmembrane #status predicted <TM6>

Query Match Score 49; DB 2; Length 31;
Best Local Similarity 47.6%; Pred. No. 18;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RMKSLAAALTYAGAMLAAPVA 23
Db 89 RLTMAVAVTASAILAFPNA 109

RESULT 10
JCl439
A:Alternate names: endo-1,3-beta-glucanase
C:Species: Hordeum vulgare (barley)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: JC1439
R:Xu, P.; Wang, J.; Fischer, G.B.
Gene 120 ; 157-165 ; 1992
A:Title: Evolution and differential expression of the (1->3)-beta-glucan endohydrolase-e
A:Reference number: JC1434; MUID:93013030; PMID:1398132
A:Status: nucleic acid sequence not shown
A:Accession: JC1439
A:Molecule type: DNA
A:Residues: 1-317 <XUP>
A:Cross-references: GB:MM96941
C:Superfamily: beta-1,3-glucanase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match Score 43.4%; Score 49; DB 2; Length 317;
Best Local Similarity 59.1%; Pred. No. 19;
Matches 13; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 4 MKSLAAALTYAGAMLAAPVA 25
Db 108 MKNLAAALQAAG--LSVPVTTA 127

RESULT 11

G71078
A:Protein: hypothetical protein PH0895 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: G71078
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuki, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene-organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: G71078
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <KAW>
A:Cross-references: UNIPROT:OS8639 ; GB:AP000004; NID:g3236131; PIDN:BAA29989.1; PID:9325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0895

RESULT 12

Query Match Score 42.5%; Score 48; DB 2; Length 106;
Best Local Similarity 31.8%; Pred. No. 9 9; Mismatches 7; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTYAGAMLAAPV 22
Db 26 LERLRLTSKIGIAGGSINSIPV 47

P95868
A:Protein: hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magapla
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: P95868
R:Flanigan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9899-9904, 2001
A:Title: The complete sequence of the 1.63-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: P95868
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q92WM3 ; GB:AL591985; PIDN:GAC48614.1; PID:G15140086 ; GSPDB:C
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Flaujan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Federspiel, N.A.; Fisher, R.F.; Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,

L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lejaire, H.; Vandembroucq, M.; Votholter, F.J.; Weidner, D.H.; Wong, K.; Yeh, K.; Reference number: A960399; MUID:21368234; PMID:11474104
A;Annotations: annotation
C;Genetics:
A;Gene: Shb20222
A;Genome: Plasmid

RESULT 13
A35259
Query Match Score 48; DB 2; Length 136;
Best Local Similarity 52.0%;
Matches 11; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
C;Species: Actinomyces viscosus
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
C;Accession: A35259
C;Keywords: transmembrane protein
R;Young, N.K.; Cisar, J.O.
J;Bacteriol. 172, 2462-2468, 1990
A;Title: Sequence homology between the subunits of two immunologically and functionally related proteins
A;Reference number: A35259; MUID:90236904; PMID:1970561
A;Accession: A35259
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-533 <YEU>
A;Cross-references: UNIPROT:P18477; GB:M32067; NID:9141049; PID:AAA62572.1; PMID:g141850
C;Keywords: transmembrane protein
P;Proc. Natl. Acad. Sci. U.S.A. 90, 7411-7413, 1993
A;Title: Cloning and characterization of a cDNA encoding glyoxal oxidase, a H-20-2-protein
A;Reference number: A48296; MUID:93348282; PMID:8346264
A;Accession: A48296
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-559 <KEP>
C;Cross-references: UNIPROT:Q011772; GB:L18991
C;Superfamily: Arabidopsis thaliana hypothetical protein FSK20_250
C;Keywords: extracellular protein; glycoprotein; oxidoreductase
P;1/22/Domain: signal sequence #status Predicted <SIG>

Query Match Score 48; DB 2; Length 559;
Best Local Similarity 52.4%;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
C;Accession: I40329
R;Fernandez, R.C.; Weiss, A.A.
Infect. Immun. 62, 4727-4738, 1994
A;Title: Cloning and sequencing of a Bordetella pertussis serum resistance locus.
A;Reference number: I40329; MUID:9012680; PMID:927748
A;Accession: I40329
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1010 <RES>
A;Cross-references: UNIPROT:Q45340; EMBL:U12276; MUID:9562025; PID:9562025
A;Genetics:
A;Gene: brxA

RESULT 14
A44296
Query Match Score 48; DB 2; Length 1010;
Best Local Similarity 52.4%;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
C;Species: Pseudomonas aeruginosa (strain PAO1)
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83415
R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, M.; Lory, S.; Olson, M.V.; Nature 406, 959-961, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83415
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-1234 <STO>
A;Cross-references: UNIPROT:Q9I202; GB:AE004610; GB:AE004091; NID:99947825; PIDN:AAG05231
A;Experimental source: strain PAO1
C;Genetics:

RESULT 15
A10329
Query Match Score 48; DB 2; Length 1010;
Best Local Similarity 52.4%;
Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
C;Species: Escherichia coli (strain C157:H7, substrain RI)

Residues: 1-98 <HAY>
A; Cross-references: UNIPROT:Q8XA78; GB:BA000007; PIDN:BAB33428.1; PID:gi1359461; GSDB:G
A; Experimental source: strain O157:H7, Substrain RIMD 050952
C; Genetics:
A; Gene: EC0005
C; Superfamily: Escherichia coli hypothetical protein b2390
Query Match Score 47.5; DB 2; Length 98;
Best Local Similarity 45.8%; Pred. No. 11;
Matches 11; Conservative 7; Mismatches 3; Indels 3; Gaps 1;
QY 1 MKRMKSIAAAITYAGAMLAAPVAT 24
DB 1 MKRQCSIVIALSLL--VLVAPM AT 21

RESULT 18
B55480
hypothetical protein Z0005 [imported] - Escherichia coli (strain O157:H7, substrate EDL9
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #text_change 09-Jul-2004
C; Accession: E85480
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimambanta, E.; Potamisis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: AB5480; PMID:21074935; PMID:12065551
A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: UNIPROT:Q8XA78; GB:ABQ05174; PIDN:gi12512680; PIDN:AAGG54305.1; GSDB:G
A; Experimental source: strain O157:H7, substrate EDL933
C; Genetics:
A; Gene: Z0005
C; Superfamily: Escherichia coli hypothetical protein b2390
Query Match Score 47.5; DB 2; Length 98;
Best Local Similarity 45.8%; Pred. No. 11;
Matches 11; Conservative 7; Mismatches 3; Indels 3; Gaps 1;
QY 1 MKRMKSIAAAITYAGAMLAAPVAT 24
DB 1 MKRQCSIVIALSLL--VLVAPM AT 21.

RESULT 19
A46414
histidine protein kinase divJ - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Feb-1998
C; Accession: A46414
R; Ohta, N.; Lane, T.; Ninfa, E.G.; Sommer, J.M.; Newton, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 10297-10301, 1992
A; Title: A histidine protein kinase homologe required for regulation of bacterial cell
A; Reference number: A46414; MUID: 93066226; PMID:1438215
A; Accession: A46414
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-596 <OH>
A; Note: Sequence extracted from NCBI backbone (NCBIN:117838, NCBIPI:117839)
C; Keywords: phosphohistidine; phosphoprotein
F; 337/Binding site: phosphate (His) (covalent) #status predicted
Query Match Score 47.5; DB 2; Length 596;
Best Local Similarity 64.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 4; Indels 5; Gaps 2;
QY 6 SIAAAIT-YAGAMLA--APVATA 25
DB 101 SIAAVLTGGGAMAAWCLAPVAAA 125

RESULT 20
CB7381
sensor histidine kinase DivJ [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: CB7381
R; Niernan, W.C.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.T.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: UNIPROT:Q03228; GB:AE005673; PIDN:ANK23047.1; GSDB:G
C; Genetics:
A; Gene: CB1063
Query Match Score 42.0%; DB 2; Length 597;
Best Local Similarity 64.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 4; Indels 5; Gaps 2;
QY 6 SIAAAIT-YAGAMLA--APVATA 25
DB 101 SIAAVLTGGGAMAAWCLAPVAAA 125

RESULT 21
AG0016
probable exported protein YP00130 [imported] - Yersinia pestis (strain CO92)
C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Accession: AG0016
C; Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 411, 522-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470013; PMID:11586360
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-89 <KUR>
A; Cross-references: UNIPROT:Q8ZJH7; GB:AL590842; PIDN:CAC88993.1; PID:gi15978235; GSDB:G
C; Genetics:
A; Gene: YP00130
Query Match Score 47.5%; DB 2; Length 89;
Best Local Similarity 43.5%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 MKRMKSIAAAITYAGAMLAAPVATA 23
DB 1 MKLKKNAVALVIGLSFAATA 23

RESULT 22
H87431
hypothetical protein CC1472 [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: H87431
R; Niernan, W.C.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.T.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Status: preliminary
A; Molecule type: DNA

A;Residues: 1-172 <STO>
 A;Cross-references: UNIPROT:Q9A890; GB:AE005673; NID:913422842; PIDN:AAK23452.1; GSPDB:G
 C;Genetics: CC1472

Query Match 41.6% Score 47; DB 2; Length 172;
 Best Local Similarity 50.0%; Pred. No. 21;
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 4 MKSLAAALTVAGMLAAPVATA 25
 Db 5 MAAVAMTVAASAAAADPMSA 26

RESULT 23
 T44619 hypothetical protein 2 [imported] - *Bacillus cereus*
 C;Species: *Bacillus cereus*
 C;Accession: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 R;Okstdt, O.A.; Hegna, I.; Lindbaek, T.; Fisched, A.L.; Kolstoo, A.B.
 Microbiology 145, 621-631, 1999
 A;Title: Genome organisation is not conserved between *Bacillus cereus* and *Bacillus subtilis*
 A;Reference number: Z22811; PMID:10217496
 A;Accession: T44619
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-173 <OKS>
 A;Cross-references: UNIPROT:Q31351; EMBL:Y11139; NID:92462114; PIDN:CAA72024.1; PID:9246
 A;Experimental source: ATCC 10987
 C;Genetics:
 A;Note: ORF2

Query Match 41.6% Score 47; DB 2; Length 173;
 Best Local Similarity 48.0%; Pred. No. 21;
 Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KMRKSLAAALTVAGMLAAPVATA 25
 Db 1 MPRLSKASLLVRSILLAPPARA 25

RESULT 24
 T35643 probable integral membrane protein - *Streptomyces coelicolor*
 C;Species: *Streptomyces coelicolor*
 C;Accession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, June 1999
 A;Reference number: Z26643
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-206 <OLI>
 A;Cross-references: UNIPROT:Q9X8Z0; EMBL:AL078610; PIDN:CAR44411.1; GSPDB:GN00070; SCOED
 C;Genetics:
 A;Gene: SCOBDB:SCH35.16

Query Match 41.6% Score 47; DB 2; Length 206;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 KRMKSLAAALTVAGMLAAPVATA 23
 Db 48 QLRRRRAALASGGMLAAVANA 69

RESULT 25
 AH3003 penicillin-binding protein dacP precursor dacP [imported] - *Agrobacterium tumefaciens* (s
 C;Species: *Agrobacterium tumefaciens*

A;Residues: 1-548 <WHI>
A;Cross-references: UNIPROT:Q9RTKB; GB:AE002017; PIDN:g6459527; NID:AE000513;
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR4752
A;Map position: 1
Query Match 41.6%; Score 47; DB 2; Length 548;
Best Local Similarity 52.2%; Pred. No. 56; Indels 9; Gaps 0;
Matches 12; Conservative 2; Mismatches 9;
Qy 3 RMKSLAAALTVAGAMLAAPVATA 25
Db 171 RYMLLAGAAGIGAVHLHPLAAA 193
A;Cross-references: UNIPROT:Q8U6T7; GB:AE008689; PIDN:AAI45513.1; PMID:11743193
A;Accession: AC3137
A;Status: Preliminary
A;Residues: 1-502 <KUR>
A;Cross-references: UNIPROT:Q8U6T7; GB:AE008689; PIDN:AAI45513.1; PMID:917743223; GSPDB:G

RESULT 28
T51189 probable ATP-dependent DNA helicase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor
C;Accession: T351189
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

R;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

A;Reference number: Z11571
A;Accession: T351189

A;Status: Preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
A;Residues: 1-719 <SEE>

A;Cross-references: UNIPROT:O69992; EMBL:AL022374; PIDN:CAA16513.1; GSPDB:GN00070; SCOED

A;Experimental source: strain A3(2)

C;Genetics:
A;Gene: SCOEDB:SCS8.05

Query Match 41.6%; Score 47; DB 2; Length 719;

Best Local Similarity 43.5%; Pred. No. 71; Mismatches 7; Indels 0; Gaps 0;

Matches 10; Conservative 6; Mismatches 7;

Qy 2 KRMKSLAAALTVAGAMLAAPVAT 24
Db 656 QRLFALASFTVPEGLAAATA 678

RESULT 29
A98151 dipeptide transporter protein dppA (truncated) [imported] - Agrobacterium tumefaciens (s

C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

R.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science, 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21606551; PMID:11743194

A;Accession: A98151
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-502 <KUR>

A;Cross-references: UNIPROT:Q8U6T7; GB:AE007870; PIDN:AAK88731.1; PID:915158470; GSPDB:G

C;Genetics:
A;Gene: ACP_L_325

A;Map position: linear chromosome

Query Match 41.2%; Score 46.5%; DB 2; Length 502;

Best Local Similarity 44.0%; Pred. No. 61; Mismatches 8; Indels 1; Gaps 1;

Matches 11; Conservative 8; Mismatches 5;

Qy 1 MKRMKSLAAALTVAGAMLAAPVATA 25
Db 1 MKKIQQTAAAL-LASAVLAVPALSS 24

RESULT 30
S14023 hypothetical protein 29 - Chlamydomonas reinhardtii transposon

C;Species: Chlamydomonas reinhardtii
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004

R;Day, A.; Rochaix, J.D.

Nucleic Acids Res., 19, 1259-1266, 1991

A;Title: A Transposon with an unusual LTR arrangement from Chlamydomonas reinhardtii con

A;Reference number: S14018; MUID:91232906; PMID:18515555
A;Accession: S14023
A;Status: Preliminary

AC3137 hypothetical protein dppA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC3137
R;Wood, D.W.; Setubal, J.C.; Kauh, R.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
erage, G.; Gillet, W.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L.
; Karp, P.; Romero, P.; Zhang, S.
Science, 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Perry, M.; Gordon-Kamm, M.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB25577; MUID:21608550; PMID:11743193
A;Accession: AC3137
A;Status: Preliminary
A;Residues: 1-502 <KUR>
A;Cross-references: UNIPROT:Q8U6T7; GB:AE008689; PIDN:AAI45513.1; PMID:917743223; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dppA
A;Map position: linear chromosome
Query Match 41.2%; Score 46.5%; DB 2; Length 502;
Best Local Similarity 41.0%; Pred. No. 61; Mismatches 8; Indels 1; Gaps 1;
Matches 11; Conservative 8; Mismatches 5;

Qy 1 MKRMKSLAAALTVAGAMLAAPVATA 25
Db 1 MKKIQQTAAAL-LASAVLAVPALSS 24

RESULT 31
H87616 cytochrome c family protein [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Accession: HB7616 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A., 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus

A;Reference number: A87249; MUID:21173698; PMID:11253647

A;Accession: HB7616
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-124 <STO>
A;Cross-references: UNIPROT:Q9A473; GB:AE005673; NID:913424600; PIDN:AAK24932.1; GSPDB:G
A;Gene: CC2970
C;Genetics:
A;Map position: linear chromosome
Query Match 40.7%; Score 46%; DB 2; Length 124;
Best Local Similarity 41.7%; Pred. No. 22; Mismatches 6;
Matches 10; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 2 KRMKSLAAALTVAGAMLAAPVATA 25
Db 5 RTIRPLAVVLLAGGLLAAGTAA 28

RESULT 32
S14023 hypothetical protein 29 - Chlamydomonas reinhardtii transposon

C;Species: Chlamydomonas reinhardtii

C;Accession: S14023
R;Day, A.; Rochaix, J.D.

Nucleic Acids Res., 19, 1259-1266, 1991

A;Title: A Transposon with an unusual LTR arrangement from Chlamydomonas reinhardtii con

A;Reference number: S14018; MUID:91232906; PMID:18515555
A;Accession: S14023
A;Status: Preliminary

Qy 4 MKSLAAALTIVAGAMILAAPVATA 25
 Db 334 LKALAAALSV-RLLGFPLATA 353

RESULT 37
 C81729 Mrp/TrxB/Tyro permease family protein TC0204 [Imported] - Chlamydia muridarum (strain Ni)
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Accession: C81729
 C;Sequence: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Saizberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A811500; PMID:10684935
 A;Accession: C81729
 A;Status: preliminary
 A;Residues: 1-398 <DNA>
 A;Cross-references: UNIPROT:Q9PRA3; GB:AE002287; GB:AE002160; NID:g7190237; PIDN:AAF3907

Query Match Score 45.5%; Pred. No. 69; Length 398;
 Best Local Similarity 46.2%;保守性 3; Mismatches 6; Indels 5; Gaps 1;

Qy 5 KSLAAALTIVAGAMILAAPVATA 25
 Db 4 KMGGALIVAGTTIGAVLAPIATS 29

RESULT 40
 A26386 hypothetical protein 402 - Streptomyces glaucescens
 C;Species: Streptomyces glaucescens
 C;Accession: A26386
 C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
 R;Huber, M.; Huetter, R.; Lorch, K.
 Nucleic Acids Res. 15, 8106, 1987
 A;Title: The promoter of the Streptomyces glaucescens mel operon.
 A;Reference number: A26386; PMID:88040431; PMID:3118334
 A;Accession: A26386
 A;Molecule type: DNA
 A;Residues: 1-134 <HUB>
 A;Cross-references: UNIPROT:P55047; GB:Y00457; NID:g46917; PIDN:CAA68512.1; PMID:946918

Query Match Score 45%; Pred. No. 32; Length 134;
 Best Local Similarity 41.4%;保守性 5; Mismatches 8; Indels 4; Gaps 1;

Qy 1 MKRMQLALITVATA---MLRVAATA 25
 Db 4 LSRRRALGAAAALAAAAGTQAVAAFAATA 32

Search completed: December 1, 2004, 11:50:55
 Job time : 40 secs

RESULT 38
 A26331 amylase precursor, extracellular - Aeromonas hydrophila
 C;Species: Aeromonas hydrophila
 C;Accession: A26331
 C;Date: 09-Sep-1988 #sequence_revision 09-Sep-1988 #text_change 16-Aug-2004
 R;Gobius, K.S.; Pemberton, J.M.
 J. Bacteriol. 170, 1325-1332, 1988
 A;Title: Molecular cloning, characterization, and nucleotide sequence of an extracellular amylase gene from *Aeromonas hydrophila*.
 A;Reference number: A26331; PMID:88139196; PMID:2449422
 A;Accession: A26331
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-464 <GOB>
 A;Cross-references: UNIPROT:P22630; GB:M20401; NID:g141869; PIDN:AAA21936.1; PMID:g141870
 C;Superfamily: Alpha-amylase; alpha-amylase core homology

Query Match Score 45.5%; Pred. No. 79; Length 464;
 Best Local Similarity 54.5%;保守性 3; Mismatches 6; Indels 1; Gaps 1;

Qy 4 MKSLAAALTIVAGAMILAAPVATA 25
 Db 1 MKNTAGILATAG-MLIAPLAHA 21

RESULT 39
 S45608 light-harvesting protein II B-800/850 alpha chain - Rhodococcus gelatinosus
 C;Species: Rhodococcus gelatinosus
 C;Date: 10-Dec-1994 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C;Accession: S45608; S66177
 R;Brunisholz, R.A.; Suter, F.; Zuber, H.
 Bur. J. Biochen. 222, 667-675, 1994
 A;Title: Structural and spectral characterisation of the antenna complexes of Rhodococcus

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OM protein - protein search, using sw model

Run on: December 1, 2004, 11:32:44 ; Search time 153 Seconds
 (without alignments)

58.616 Million cell updates/sec

Title: US-10-673-860-3

Perfect score: 113
 Sequence: 1 MKRKSLLAALTYAGAMLAAPVATA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : A_Geneseq_23Sep04:
 1: geneseqP1980s: *
 2: geneseqP1990s: *
 3: geneseqP2000s: *
 4: geneseqP2001s: *
 5: geneseqP2002s: *
 6: geneseqP2003s: *
 7: geneseqP2004s: *
 8: geneseqP2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	113	100.0	25	4	AAB81158	SPa Pept
2	113	100.0	25	6	ABU07388	Corynefor
3	113	100.0	25	7	ADW64923	Corynebac
4	113	100.0	358	2	ADW56155	Aa_Cells
5	57	50.4	395	4	AAG94890	Hag92890 C glutami
6	51	45.1	104	4	AAG91111	C glutami
7	51	45.1	107	2	AAW32371	Mycobacte
8	51	45.1	107	2	AAW32439	Mycobacte
9	51	45.1	107	2	AAW64311	Mycobacte
10	51	45.1	107	2	AAW81674	M. tuberc
11	51	45.1	107	2	AAV38976	M. tuberc
12	51	45.1	107	2	AAV39113	M. tuberc
13	51	45.1	168	2	AAW32393	Mycobacte
14	51	45.1	168	2	AAW32465	Mycobacte
15	51	45.1	168	2	AAW64332	Mycobacte
16	51	45.1	168	2	AAW81699	M. tuberc
17	51	45.1	168	2	AAV38986	M. tuberc
18	51	45.1	168	2	AAV39129	M. tuberc
19	51	45.1	168	4	AAB52454	Mycobacte
20	51	45.1	168	5	ABU05883	M. tuberc
21	51	45.1	186	2	AAW32351	Mycobacte
22	51	45.1	186	2	AAW32419	Mycobacte
23	51	45.1	186	2	AAW81654	M. tuberc
24	51	45.1	187	2	AAW64291	Mycobacte
25	51	45.1	187	2	AAV38956	M. tuberc

WO200123591-A1.

PN

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PD

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PP

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PR

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PR

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OS

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Claim 7; Page 77; 151pp; Japanese.

This invention relates to a process for the production of a foreign secretory protein through the construction of a recombinant coryneform bacterium. The coryneform bacterium is transformed with an expression construct in which DNA encoding a target foreign protein pro-structure is ligated to the downstream region of DNA encoding the signal peptide domain of a coryneform bacterial protein. Following transformation with the vector, the bacterium is cultured, and the pro-peptide cleaved from the expressed protein. Transglutaminases produced using this process are useful in the food processing and pharmaceutical industries. The present sequence represents a Corynebacterium ammonigenes SPa peptide, which is used in the method of the invention.

XX PS Claim 17; SEQ ID NO 6644; 246pp + Sequence Listing; English.

XX XX The present invention provides a number of nucleotide and protein

XX CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

XX CC are useful for identifying the mutation point of a gene derived from a

XX CF mutant of coryneform bacterium, measuring expression amount and analysing

XX CC the expression profile or expression pattern of a gene derived from a

XX DR coryneform bacterium, and identifying a homologue of a gene derived from

XX CC coryneform bacterium. Coryneform bacteria are useful for producing amino

XX CC acids, nucleic acids, vitamins, saccharides and organic acids.

XX PA (AJIN) AJINOMOTO KK.

XX DR WPI : 1998-304970/27.

XX N-PADB; AAV22667.

XX PT New DNA isolated from Corynebacterium ammoniagenes encodes cell surface

PT PR layer protein - and recombinant DNA, vector and host used to produce

PR protein.

XX PS Claim 1; Page 5-7; 8pp; Japanese.

XX CC The present sequence represents a cell surface layer protein, and is

CC isolated from Corynebacterium ammoniagenes ATCC6872. A gene of interest

CC can be inserted downstream of the present sequence. Subsequent expression

CC of the gene by the microbe causes it to be secreted extracellularly

XX SQ Sequence 358 AA;

RESULT 6

Query Match	100.0%	Score 113;	DB 2;	Length 358;
Best Local Similarity	100.0%	Pred. No. 3 1e-09;		
Matches	25;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps 0;		

XX ID AAG91111 standard; protein: 104 AA.

XX XX ID AAG91111.

XX AC AAG91111;

XX DT 26-SEP-2001 (first entry)

XX DE C glutamicum protein fragment SEQ ID NO: 4865.

XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

XX KW organic acid synthesis.

XX OS Corynebacterium glutamicum.

XX PN EP1108790-A2.

XX PD 20-JUN-2001.

XX PP 18-DEC-2000; 2000EP-00127688.

XX PR 16-DEC-1999; 99JP-00377484.

XX PR 07-APR-2000; 2000JP-00159162.

XX PR 03-AUG-2000; 2000JP-00280988.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX XX WPI ; 2001-376931/40.

XX DR N-PSDB; AAH66310.

XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analyzing

PT expression profile or pattern of a gene and identifying homologous gene.

XX PS Claim 17; SEQ ID NO 4865; 245pp + Sequence Listing; English.

XX XX The present invention provides a number of nucleotide and protein

XX CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

XX CC are useful for identifying the mutation point of a gene derived from a

XX DR mutant of coryneform bacterium, measuring expression amount and analysing

XX CC the expression profile or expression pattern of a gene derived from a

XX DR coryneform bacterium, and identifying a homologue of a gene derived from

XX CC coryneform bacterium. Coryneform bacteria are useful for producing amino

XX CC acids, nucleic acids, vitamins, saccharides and organic acids,

XX CC acids, nucleic acids, vitamins, saccharides and organic acids,

CC particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.

XX Sequence 104 AA;

Query Match 45.1%; Score 51; DB 4; Length 104;
Best Local Similarity 48.0%; Pred. No. 9.7.
Matches 12; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MRKMKSLAAALTVAGAMIAAPVATA 25
Db 2 IKKYLSTIAAVTIAASAVLFAAPSQA 26

RESULT 7

ID AAW32371 standard; protein; 107 AA.
XX
AC AAW32371;
XX DT 13-JAN-1998 (first entry)
DB Mycobacterium tuberculosis antigen TbRaB.
XX KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
KW skin testing; M.tuberculosis.
OS Mycobacterium tuberculosis.
XX

Key Location/Qualifiers

FT Misc-difference 60 /note= "Any amino acid"
FT Misc-difference 64 /note= "Any amino acid"
FT Misc-difference 73 /note= "Any amino acid"
FT Misc-difference 77 /note= "Any amino acid"
FT Misc-difference 79 /note= "Any amino acid"
FT Misc-difference 86 /note= "Any amino acid"
FT Misc-difference 99 /note= "Any amino acid"
FT Misc-difference 102 /note= "Any amino acid"
FT Misc-difference 102 /note= "Any amino acid"
FT Misc-difference 103 /note= "Any amino acid"
FT Misc-difference 106 /note= "Any amino acid"
FT Misc-difference 106 /note= "Any amino acid"
XX WO9709429-A2.
PN (CORI-) CORIXA CORP.
PD 13-MAR-1997.
XX 30-AUG-1996; 96KO-US014675.
XX 01-SEP-1995; 95US-00523435.
PR 22-SEP-1995; 95US-00532136.
PR 22-MAR-1996; 96US-00620280.
PR 05-JUN-1996; 96US-00058800.
PR 12-JUL-1996; 96US-00680573.
XX

Reed SG, Skeiky YAN, Dillon DC, Campos-Neto A, Houghton R;
PI Vedick TH, Twarzik DR;
XX

WPI; 1997-192904/17.
N-PSDB; AAT91418.
XX

PT New immunogenic polypeptide(s) from soluble M. tuberculosis antigens -
PT useful for diagnosis of M. tuberculosis infection.

XX Example 3; Page 131-132; 190pp; English.

XX A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbRaB. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.

CC SQ Sequence 107 AA;

Query Match 45.1%; Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRKMKSLAAALTVAGAMIAAPVATA 20
Db 10 MRKVSIAGAGTTAAAGIGAA 29

RESULT 8

AAW32439 standard; protein; 107 AA.
XX
ID AAW32439
XX AC AAW32439;
XX DT 08-JAN-1998 (first entry)
XX DE Mycobacterium tuberculosis antigen TbRaB.
XX KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
KW skin testing; M.tuberculosis.
OS Mycobacterium tuberculosis.
XX
Key Location/Qualifiers
FH
FT Misc-difference 60 /note= "Any amino acid"
FT Misc-difference 64 /note= "Any amino acid"
FT Misc-difference 73 /note= "Any amino acid"
FT Misc-difference 77 /note= "Any amino acid"
FT Misc-difference 79 /note= "Any amino acid"
FT Misc-difference 86 /note= "Any amino acid"
FT Misc-difference 99 /note= "Any amino acid"
FT Misc-difference 102 /note= "Any amino acid"
FT Misc-difference 103 /note= "Any amino acid"
FT Misc-difference 106 /note= "Any amino acid"
FT Misc-difference 106 /note= "Any amino acid"
XX
FT Misc-difference 99 /note= "Any amino acid"
FT Misc-difference 102 /note= "Any amino acid"
FT Misc-difference 64 /note= "Any amino acid"
FT Misc-difference 73 /note= "Any amino acid"
FT Misc-difference 77 /note= "Any amino acid"
FT Misc-difference 79 /note= "Any amino acid"
FT Misc-difference 86 /note= "Any amino acid"
FT Misc-difference 99 /note= "Any amino acid"
FT Misc-difference 102 /note= "Any amino acid"
FT Misc-difference 103 /note= "Any amino acid"
FT Misc-difference 106 /note= "Any amino acid"
XX
PN WO9709428-A2.
XX PD 13-MAR-1997.
XX 30-AUG-1996; 96KO-US014674.
XX 01-SEP-1995; 95US-00523436.
PR 22-SEP-1995; 95US-00532134.
PR 22-MAR-1996; 95US-0053634.
PR 05-JUN-1996; 96US-000588074.
PR 12-JUL-1996; 96US-00680573.
XX
PR 22-MAR-1996; 96US-00620874.

PR 05-JUN-1996; 96US-00659634;
PR 12-JUL-1996; 96US-00680574.
XX (CORI-) CORIXA CORP.

XX Reed SG, Skeiky YA, Dillon DC, Campos-Neto A, Houghton R;
PI Vedvick TH, Twardzik DR;
XX WPI; 1997-192903-17.
DR N-PSDB; AAT9481.

PR New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis.
XX Example 3; Page 120; 168pp; English.
PS XX
CC A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M. tuberculosis antigen, TbRaB. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M. tuberculosis (for treatment or prevention)
CC Sequence 107 AA;
SQ Query Match Similarity 45.1%; Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Prd. No. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Db 1 MKRMKSLLAAALTVAGAMLA 20
10 MKMVKSIAGLTAAGAA 29

RESULT 9
ID AAW64311 standard; protein; 107 AA.
XX AAW64311;
AC
XX DT 17-OCT-2003 (revised)
DT 09-NOV-1998 (first entry)
XX DE Mycobacterium tuberculosis antigen TbRaB.
XX KW Tuberculosis; infection; diagnosis; antigen; TbRaB.
XX OS Mycobacterium tuberculosis; strain H37Ra.
XX Key Location/Qualifiers
FT Misc-difference 40 /note= "encoded by GGN"
FT Misc-difference 50 /note= "encoded by GAN"
FT Misc-difference 64 /note= "encoded by AGN"
FT Misc-difference 73 /note= "encoded by AGN"
FT Misc-difference 77 /note= "encoded by AGN"
FT Misc-difference 79 /note= "encoded by GGN"
FT Misc-difference 86 /note= "encoded by GNG"
FT Misc-difference 89 /note= "encoded by GGN"
FT Misc-difference 94 /note= "encoded by GGN"
FT Misc-difference 95 /note= "encoded by GGN"

FT Misc-difference 97 /note= "encoded by GGN"
FT Misc-difference 99 /note= "encoded by GGN"
FT Misc-difference 101 /note= "encoded by ANC"
FT Misc-difference 102 /note= "encoded by GGN"
FT Misc-difference 103 /note= "encoded by GNG"
FT Misc-difference 104 /note= "encoded by NAT"
FT Misc-difference 106 /note= "encoded by GGN"
FT Misc-difference 107 /note= "encoded by NCA"
XX PN WO9816645-A2.
XX PD 23-APR-1998.
XX PF 07-OCT-1997; 97WO-US018214.
XX PR 11-OCT-1996; 96US-00729622.
XX PR 13-MAR-1997; 97US-00818111.
XX PA (CORI-) CORIXA CORP.
XX Reed SG, Skeiky YA, Dillon DC, Campos-Neto A, Houghton R;
PI Vedwick TS, Twardzik DR, Lodes MJ,
XX WPI; 1998-251292/22.
DR N-PSDB; AAV44359.
XX New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
XX Example 3; Page 120; 250pp; English.
PS XX
CC This polypeptide comprises Mycobacterium tuberculosis soluble antigen CC TbRaB. It is encoded by a DNA sequence (see AAW4359) isolated from a M. CC tuberculosis strain H37Ra expression library with rabbit anti-sera raised CC against M. tuberculosis supernatant. The invention relates to compositions and methods for diagnosing tuberculosis. It provides CC polypeptides (see AAW64311-W64179), comprising an antigenic portion of a CC soluble M. tuberculosis antigen, as well as DNA sequences encoding such CC polypeptides, recombinant expression vectors and transformed or CC transfected host cells. Also claimed are methods and diagnostic kits for CC detecting M. tuberculosis infection in a patient using the above CC polypeptides, antibodies, or oligonucleotide probes and primers, for the CC diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS CC field)
XX Sequence 107 AA;
SQ Query Match Similarity 45.1%; Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MKRMKSLLAAALTVAGAMLA 20
Db 10 MKMVKSIAGLTAAGAA 29
RESULT 10
AAW81674
ID AAW81674 standard; protein; 107 AA.
XX AC AAW81674;
XX DT 27-JAN-1999 (First entry)
XX

XX 18-FEB-1998; 98US-00025197.
PR 05-MAY-1998; 98US-00072967.
XX (CORTI-) CORIXA CORP.

XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedwick TH, Twardzik DR, Lodes MJ, Hendrickson RC;
XX WPI; 1999-527409/44.
DR N-PSDB; AAZ19269.
XX New antigens from Mycobacterium tuberculosis useful in diagnostic skin
tests and protective or therapeutic vaccines or compositions.
PR Example 3; Page 111; 299pp; English.
XX The present invention describes polypeptides comprising an immunogenic
part of a Mycobacterium tuberculosis antigen (Ag). Also described are
vaccines and fusion protein containing M. tuberculosis Ag's. M.
tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other
polypeptides fragments, can be used in pharmaceutical compositions or
vaccines to generate a protective or therapeutic immune response to M.
tuberculosis and as reagents in skin tests for diagnosis of tuberculosis.
Ag can induce proliferation of, or cytokine secretion by, T, B or natural
killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249
to AAZ19460 and AAY39083 to AAY39225 are used in the exemplification of
the present invention
XX Sequence 107 AA;

Query Match Score 51; DB 2; Length 107;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MKRMKSLAAALTYAGAMLA 20
Db 10 MRNVSIAAGLTAAAIGAA 29

RESULT 13
AAW32393 ID AAW32393 standard; protein; 168 AA.
XX AAW32393;
XX DT 12-JAN-1998 (first entry)
DE Mycobacterium tuberculosis antigen DPAS.
XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
KW skin testing; M.tuberculosis.
XX OS Mycobacterium tuberculosis.
XX PN WO9709429-A2.
PD 13-MAR-1997.
XX 30-AUG-1996; 96WO-US014674.
DE Mycobacterium tuberculosis.
XX PR 01-SEP-1995; 95US-0053436.
PR 02-SEP-1995; 95US-0053436.
PR 22-MAR-1996; 96US-0052080.
PR 05-JUN-1996; 96US-0058800.
PR 12-JUL-1996; 96US-00680573.
XX (CORTI-) CORIXA CORP.
PA Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
PI Vedwick TH, Twardzik DR;
XX WPI; 1997-19203/17.
DR N-PSDB; AAT9187.
XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
useful in vaccines for prevention or treatment of tuberculosis, also for
diagnosis.
XX Disclosure; Page 132-133; 168pp; English.
PR WPI; 1997-192904/17.

A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, DPAS. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention)

SQ Sequence 168 AA;

Query Match 45.1%; Score 51; DB 2; Length 168;

Best Local Similarity 60.0%; Pred. No. 17; Mismatches 5; Indels 0; Gaps 0;

ID AAW81699 standard; protein; 168 AA.

Db 1 MKRMKSIAAALTVAGMLAA 20

SQ 1 MKMVKSIAAGLTAAAIGAA 20

RESULT 16

Best Local Similarity 60.0%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;

ID AAW81699 standard; protein; 168 AA.

Db 1 MKMVKSIAAGLTAAAIGAA 20

RESULT 15

AAW64332 standard; protein; 168 AA.

AC AAW64332;

XX 17-OCT-2003 (revised)

DT 09-NOV-1998 (first entry)

XX Mycobacterium tuberculosis antigen DPAS.

DB Tuberculosis; infection; diagnosis; antigen; DPAS.

XX Mycobacterium tuberculosis; strain H37Rv.

OS WO9816645-A2.

PN 23-APR-1998.

PD XX 07-OCT-1997; 97WO-US018293.

XX PR 11-OCT-1996; 96US-00730510.

XX PR 13-MAR-1997; 97US-00818112.

XX DR (CORI-) CORIXA CORP.

PA XX PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;

XX PI Veddick TS, Twardzik DR, Lodes MJ;

XX PR XX WPI; 1998-261042/23.

DR N-PSDB; AAV64499.

XX PA Disclosure; Page 124; 230pp; English.

XX PT This sequence represents an immunogenic portion of a soluble

CC Mycobacterium tuberculosis (MT) antigen which can be used in a method for

CC developing protective immunity against tuberculosis (TB). This sequence can

CC be formulated into vaccines and/or pharmaceutical compositions for

CC immunizing against M. tuberculosis infection or may be used for the

CC diagnosis of tuberculosis.

XX PS Example 1; Page 128; 250pp; English.

XX This polypeptide comprises the Mycobacterium tuberculosis antigen DPAS. A DNA sequence (see AAV4391) coding for DPAS was isolated from a M. tuberculosis genomic library. An N-terminal peptide (see AAW64346) of DPAS was shown to induce proliferation and interferon-gamma production in peripheral blood mononuclear cells. DPAS shows sequence homology to a Mycobacterium leprae protein. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW6429-L-W64319) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also

CC claimed are methods and diagnostic kits for detecting M. tuberculosis

CC infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.

CC (Updated on 17-OCT-2003 to standardise OS field)

CC XX Sequence 168 AA;

CC SQ Query Match 45.1%; Score 51; DB 2; Length 168;

CC Best Local Similarity 60.0%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;

CC Matches 12; Conservative

CC Qy 1 MKRMKSIAAALTVAGMLAA 20

CC Db 1 MKMVKSIAAGLTAAAIGAA 20

RESULT 16

Best Local Similarity 60.0%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;

ID AAW81699 standard; protein; 168 AA.

Db 1 MKMVKSIAAGLTAAAIGAA 20

RESULT 15

AAW64332 standard; protein; 168 AA.

AC AAW64332;

XX 17-OCT-2003 (revised)

DT 09-NOV-1998 (first entry)

XX Mycobacterium tuberculosis antigen DPAS.

DB Tuberculosis; infection; diagnosis; antigen; DPAS.

XX OS Mycobacterium tuberculosis; strain H37Rv.

PN WO9816645-A2.

PN 23-APR-1998.

PD XX 07-OCT-1997; 97WO-US018293.

XX PR 11-OCT-1996; 96US-00730510.

XX PR 13-MAR-1997; 97US-00818112.

XX DR (CORI-) CORIXA CORP.

PA XX PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;

XX PI Veddick TS, Twardzik DR, Lodes MJ;

XX PR XX WPI; 1998-261042/23.

DR N-PSDB; AAV64499.

XX PA Disclosure; Page 124; 230pp; English.

XX PT This sequence represents an immunogenic portion of a soluble

CC Mycobacterium tuberculosis (MT) antigen which can be used in a method for

CC developing protective immunity against tuberculosis (TB). This sequence can

CC be formulated into vaccines and/or pharmaceutical compositions for

CC immunizing against M. tuberculosis infection or may be used for the

CC diagnosis of tuberculosis.

XX PS Example 1; Page 128; 250pp; English.

XX This polypeptide comprises the Mycobacterium tuberculosis antigen DPAS. A DNA sequence (see AAV4391) coding for DPAS was isolated from a M. tuberculosis genomic library. An N-terminal peptide (see AAW64346) of DPAS was shown to induce proliferation and interferon-gamma production in peripheral blood mononuclear cells. DPAS shows sequence homology to a Mycobacterium leprae protein. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW6429-L-W64319) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also

CC claimed are methods and diagnostic kits for detecting M. tuberculosis

CC infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.

XX SQ Sequence 168 AA;

XX PT Query Match 45.1%; Score 51; DB 2; Length 168;

CC Best Local Similarity 60.0%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;

CC Matches 12; Conservative

CC Qy 1 MKRMKSIAAALTVAGMLAA 20

CC Db 1 MKMVKSIAAGLTAAAIGAA 20

RESULT 17

AAV38986 standard; protein; 168 AA.

XX ID AAV38986

AC AAY38996; PR 18-FEB-1998; 98US-00025197.
 XX PR 05-MAY-1998; 98US-00072967.
 DT XX
 DE M. tuberculosis recombinant antigen protein DPAs.
 XX PA (CORI-) CORIXA CORP.
 KW Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 KW Veddick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
 KW vaccine; immunity.
 XX DR WPI: 1999-527409/44.
 OS N-PSDB; AAZ19301.
 XX PT New antigens from Mycobacterium tuberculosis useful in diagnostic skin
 PN tests and protective or therapeutic vaccines or compositions.
 XX PT
 PD Disclosure: Page 118-119; 299pp; English.
 XX
 PF 17-FEB-1999; 99WO-US003265.
 XX PR 18-FEB-1998; 98US-00024753.
 PR 05-MAY-1998; 98US-00072596.
 XX PA (CORI-) CORIXA CORP.
 XX PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Veddick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
 PI WPI: 1999-527416/44.
 DR N-PSDB; AAZ19089.
 XX PT New polypeptide comprising antigenic portions of M. tuberculosis.
 XX PS Claim 3; Page 163-164; 323pp; English.
 XX This invention describes novel recombinant antigens and their encoding
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel
 CC polypeptides are useful for detecting M. tuberculosis infection in a
 CC biological sample by detecting antibodies which bind with the
 CC polypeptides, and are useful as vaccines for immunizing against M.
 CC tuberculosis infection. The new detection methods are needed as current
 CC vaccination strategies do not provide 100% immunity.
 XX Sequence 168 AA;
 PS Query Match 45.1%; Score 51; DB 2; Length 168;
 CC Best Local Similarity 60.0%; Pred. No. 17;
 CC Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 CC
 QY 1 MKRMKSLAAALTVGAMLLAA 20
 DB 1 MKMVKSIAGLTAANAGAA 20
 XX RESULT 19
 AAB52454 ID AAB52454 standard; protein; 168 AA.
 XX AC AAB52454;
 XX DT 23-FEB-2001 (first entry)
 DE 1 MKRMKSLAAALTVGAMLLAA 20
 DE 1 MKMVKSIAGLTAANAGAA 20
 XX Mycobacterium tuberculosis secreted protein #19.
 KW Mycobacterium tuberculosis secreted protein, MTSB; vaccine.
 XX OS
 XX PN WO200666143-A1.
 XX PD 09-NOV-2000.
 XX PR 04-MAY-2000; 2000WO-US012197.
 XX DE 04-MAY-1999; 99US-0132479P.
 XX PR 04-MAY-1999; 99US-0132503P.
 XX PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
 XX PI Gennaro ML, Gomez MJ;
 XX DR WPI; 2001-007151/01.
 XX PT Novel Mycobacterium tuberculosis secreted polypeptides and
 XX PT nucleotides useful in diagnosis, treatment and prophylaxis of
 XX PT tuberculosis.
 XX PS Claim 11; Fig 1; 60pp; English.

AC AAY39129; PR 05-NOV-1999 (first entry)
 XX DE M. tuberculosis antigen DPAs amino acid sequence.
 XX KW Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
 KW immunotherapy; diagnosis; immunisation; vaccine; infection;
 KW immune response; skin test.
 OS Mycobacterium tuberculosis.
 XX PN WO942076-A2.
 XX PD 26-AUG-1999.
 XX PR 17-FEB-1999; 99WO-US003268.

XX The present invention relates to Mycobacterium tuberculosis secreted
 CC proteins (MtbP), where the polypeptide has M. tuberculosis specific
 CC antigenic and immunogenic properties. Compositions of the invention may
 CC be useful for diagnosing Mycobacterium tuberculosis infection and as a
 CC vaccine against M. tuberculosis infection.
 XX Sequence 168 AA;

XX Query Match 45.1%; Score 51; DB 4; Length 168;
 CC Best Local Similarity 60.0%; Pred. No. 17;
 Matches 12; Conservative 3; Mismatches 5;
 Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTVGAGMLAA 20
 Db 1 MKRVSIAAGLTAAGAA 20

RESULT 21
 AAW32351
 ID AAW32351 standard; protein; 186 AA.
 XX
 AC AAW32351;
 DT 13-JAN-1998 (first entry)
 DE Mycobacterium tuberculosis antigen Tbra1.
 KW Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
 KW skin testing; M.tuberculosis.
 OS Mycobacterium tuberculosis.
 PN WO9709429-A2.
 XX
 DT 13-MAR-1997.
 PD 13-MAR-1997.
 XX
 DE 30-AUG-1996;
 PR 96WO-US014675.
 XX
 DE 08-APR-2003 (first entry)
 PR 01-SEP-1995;
 KW 95US-00523435.
 KW mycobacterioses; survival; virulence; protective antigen; vaccine;
 KW mycobacterial disease; tuberculosis; leprosy.
 XX
 PR 22-SEP-1995;
 OS 96US-00620280.
 PR 22-MAR-1996;
 OS 96US-00658800.
 PR 05-JUN-1996;
 XX
 PR 12-JUL-1996;
 PA (CORI-X) CORIXA CORP.
 XX
 PR Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedrick TH, Twardzik DR;
 XX
 PR N-PSPB; AAT91401.
 XX
 PT New immunogenic polypeptide(s) from soluble M. tuberculosis antigens -
 XX
 PS Example 3; Page 99-100; 190pp; English.
 XX
 XX
 CC A new immunogenic polypeptide has been developed comprising an
 CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
 CC variant differing only in conservative substitutions and/or
 CC modifications). The present sequence represents M.tuberculosis antigen,
 CC Tbra1. The immunogenic polypeptide can be used to diagnose M.tuberculosis
 CC infection by forming complexes with specific antibodies in the sample.
 CC Fragments of DNA encoding the immunogenic polypeptide can be used as
 CC diagnostic primers or probes and agents that bind to the antigen,
 CC especially monoclonal antibodies or equivalent polyclonal antibodies, are
 CC also used for diagnosis
 XX
 SQ Sequence 186 AA;

XX Query Match 45.1%; Score 51; DB 2; Length 186;
 CC Best Local Similarity 60.0%; Pred. No. 19;
 Matches 12; Conservative 3; Mismatches 5;
 Indels 0; Gaps 0;
 Qy 1 MKRMKSLAAALTVGAGMLAA 20
 Db 20 MKRVSIAAGLTAAGAA 39

RESULT 22
 AAW32419
 ID AAW32419 standard; protein; 186 AA.

XX Sequence 168 AA;

XX Query Match 45.1%; Score 51; DB 5; Length 168;
 CC Best Local Similarity 60.0%; Pred. No. 17;

CC

CC

CC This invention relates to a novel method for identifying essential genes
 CC by a comparative genomic analysis of the sequences of Mycobacterium
 CC tuberculosis and M. leprae.

CC Claim 17; Page 744; 874pp; English.
 CC

CC Identifying and selecting genes for survival or virulence of mycobacteria
 CC PT by a comparative genomic analysis of the sequences of Mycobacterium
 CC tuberculosis and M. leprae.

CC XX
 CC This invention relates to a novel method for identifying essential genes
 CC PT for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a
 CC polynucleotide sequence that is highly conserved in both genomes with no
 CC counterparts in other bacterial species and that corresponds to
 CC an essential gene for the survival or virulence of mycobacterium species.
 CC The method of the invention is useful for detecting M. tuberculosis or M.
 CC leprae infection. The method reduces the number of potential new targets
 CC and protective antigens for new drugs and vaccine compositions to treat
 CC and prevent mycobacterial diseases, particularly tuberculosis and
 CC leprosy. The present sequence represents a marker protein from
 CC Mycobacterium tuberculosis and Mycobacterium leprae identified using the
 CC method of the invention
 XX

CC Sequence 168 AA;

XX Query Match 45.1%; Score 51; DB 2; Length 186;
 CC Best Local Similarity 60.0%; Pred. No. 19;
 Matches 12; Conservative 3; Mismatches 5;
 Indels 0; Gaps 0;

Qy 1 MKRMKSLAAALTVGAGMLAA 20
 Db 20 MKRVSIAAGLTAAGAA 39

AC AAW32419;
 XX
 DT 08-JAN-1998 (first entry)
 XX Mycobacterium tuberculosis antigen TbRaI.
 DE Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
 KW skin testing; M. tuberculosis.
 XX
 OS Mycobacterium tuberculosis.
 XX WO9709428-A2.
 XX
 PD 13-MAR-1997.
 XX
 PF 30-AUG-1996; 96WO-US014674.
 XX
 PR 01-SEP-1995; 95US-00523436.
 PR 22-SEP-1995; 95US-00533334.
 PR 05-MAR-1996; 96US-00620874.
 PR 05-JUN-1996; 96US-00659633.
 PR 12-JUL-1996; 96US-00680574.
 XX
 PA (CORI-) CORIXA CORP.
 PR Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedwick TS, Twardzik DR, Lodes MJ;
 XX WPI; 1998-261042/23.
 N-PSDB; AAV6447.

This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.

Example 3 ; Page 95; 230pp; English.

Sequence 186 AA;

Query Match Score 51; DB 2; Length 186;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKRMKSLAAALTVAAGMLAA 20
 Db 20 MKMVKSLAAAGLTAAGAIGAA 39

RESULT 24
 AAW64291 ID AAW64291 standard; protein; 187 AA.
 AC AAW64291;
 AC
 XX DT 17-OCT-2003 (revised)
 DT 09-NOV-1998 (first entry)
 XX Mycobacterium tuberculosis antigen TbRaI.
 DE Mycobacterium tuberculosis antigen TbRaI.
 XX
 KW Tuberculosis; infection; diagnosis; antigen; TbRaI.
 XX OS Mycobacterium tuberculosis; strain H37Ra.
 PH Key Location/Qualifiers
 FT Misc-difference 187 /note= "encoded by NAA"
 FT XX
 PN WO9816646-A2.
 XX
 PD 23-APR-1998.
 XX
 PF 07-OCT-1997; 97WO-US018293.
 XX PR 11-OCT-1996; 96US-00730510.
 PR 13-MAR-1997; 97US-00818112.
 XX PA (CORI-) CORIXA CORP.
 PR Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedwick TS, Twardzik DR, Lodes MJ;

RESULT 23
 ID AAW31654 Standard; protein; 186 AA.
 XX
 AC AAWB1654;
 XX
 DT 27-JAN-1999 (first entry)
 XX
 DE M. tuberculosis immunogenic polypeptide TbRaI.
 KW Tuberculosis; immunogen; soluble; antigen; protective immunity; TB;
 KW vaccine; pharmaceutical; infection; diagnosis.
 XX OS Mycobacterium tuberculosis.

Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Query 1 MKRMKSLAAATTAGMLAA 20
 Db 20 MKMKVSKTAGLTTAAAGAA 39

RESULT 27
 ABP35261 ABP35261 Standard; protein; 56 AA.

AC AC
 XX XX
 DT 08-JUL-2002 (first entry)

DE Human ORF4234 protein, SEQ ID NO:8468.

XX Human; ORF; open reading frame; ORF; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibitor; chemotaxis; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibitor; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnerability;
 KW vasotropic; antiproliferative; antidiabetic; cytostatic; nootropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW dermatological; analgesic; immunomodulator; fungicide.
 XX Homo sapiens.

OS WO20010366-A2.

PN XX
 PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US017076.

XX PR 24-MAY-2000; 2000US-0206690P.

XX PA (CURA-) CURAGEN CORP.

PI Leach MD, Shimkets RA;

XX WPI: 2002-106200/14.
 DR N-PDB; ABN79287.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation.

XX Claim 10; Page 2360; 2508pp; English.

CC Sequences ABP31028-ABP315561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN9587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF534 (collectively
 CC referred to as ORF) proteins, polynucleotides at least 85% identical to
 CC the ORF nucleic acid sequences, vectors and host cells comprising ORF
 CC polynucleotides, the recombinant production of ORF proteins, antibodies
 CC specific for ORF proteins, methods of detecting ORF polynucleotides and
 CC polypeptides, methods of screening for modulators of ORF expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORF-associated disorder. The ORF proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haemopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibit activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORF proteins,

CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORF nucleic acids may also be used as a
 CC source of primers and probes in the detection of ORF genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORF
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORF
 CC protein, and in drug screening. The ORF proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORF-associated diseases

XX Sequence 56 AA:
 SQ AAG90188 standard; protein; 279 AA.
 ID AAG90188
 XX AAG90188;
 AC AAG90188;
 DT 26-SEP-2001 (first entry)
 XX C glutamicum protein fragment SEQ ID NO: 3942.
 DE C glutamicum
 XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX Corynebacterium glutamicum.
 OS EP1108790-A2.
 PN 20-JUN-2001.
 XX PP 18-DEC-2000; 2000EP-00127688.
 XX PR 16-DEC-1999; 99JP-00377484.
 XX PR 07-APR-2000; 2000JP-00139162.
 PR 03-AUG-2000; 2000JP-00200988.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoii H;
 PI Tateishi N, Sanoh A, Ikeda M, Ozaki A;
 XX WPI; 2001-376931/40.
 DR N-PDSE; AAH65407.
 XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT the mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX WPI; 2001-376931/40.
 DR N-PDSE; AAH65407.
 XX PS Claim 17; SEQ ID NO 3942; 2465p + Sequence listing; English.
 XX The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC sequences are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and analysing
 CC the expression profile or expression pattern of a gene derived from
 CC coryneform bacterium, and identifying a homologue of a gene derived from
 CC coryneform bacterium, and identifying a homologue of a gene derived from

CC coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids.

CC particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office

XX Sequence 279 AA;

Query Match 44.2%; Score 50; DB 4; Length 279;
Best Local Similarity 48.0%; Pred. No. 41;
Matches 12; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

AC ADM20157;
XX
AC ADM20157 standard; protein; 248 AA.
XX 20-MAY-2004 (first entry)

DE Protein encoded by novel human channel/transporter gene #268 clone 2.
XX immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiotropic; vasoconstrictive; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW gene therapy; channel/transporter protein; rheumatoid arthritis;
KW neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.

XX Homo sapiens.

PN WO/00154472-A2.
XX 02-AUG-2001.

PF 17-JAN-2001; 2001MO-US001307.

XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-01980123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216644P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-021788P.
PR 14-JUL-2000; 2000US-0217496P.
PR 26-JUL-2000; 2000US-02218290P.
PR 26-JUL-2000; 2000US-02220961P.
PR 14-AUG-2000; 2000US-0224510P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.

PR PR 14-AUG-2000; 2000US-0225757P.
PR PR 14-AUG-2000; 2000US-0225758P.
PR PR 14-AUG-2000; 2000US-0225759P.
PR PR 18-AUG-2000; 2000US-022679P.
PR PR 22-AUG-2000; 2000US-0226681P.
PR PR 22-AUG-2000; 2000US-0226682P.
PR PR 22-AUG-2000; 2000US-0227678P.
PR PR 23-AUG-2000; 2000US-022709P.
PR PR 30-AUG-2000; 2000US-0228924P.
PR PR 01-SEP-2000; 2000US-0229787P.
PR PR 01-SEP-2000; 2000US-0229943P.
PR PR 01-SEP-2000; 2000US-0229944P.
PR PR 01-SEP-2000; 2000US-0229945P.
PR PR 05-SEP-2000; 2000US-0229909P.
PR PR 05-SEP-2000; 2000US-023113P.
PR PR 06-SEP-2000; 2000US-0230437P.
PR PR 06-SEP-2000; 2000US-0230438P.
PR PR 08-SEP-2000; 2000US-0231242P.
PR PR 08-SEP-2000; 2000US-0231243P.
PR PR 08-SEP-2000; 2000US-0231444P.
PR PR 08-SEP-2000; 2000US-0231413P.
PR PR 08-SEP-2000; 2000US-0231414P.
PR PR 08-SEP-2000; 2000US-0231480P.
PR PR 12-SEP-2000; 2000US-0231968P.
PR PR 12-SEP-2000; 2000US-0231977P.
PR PR 14-SEP-2000; 2000US-0233398P.
PR PR 14-SEP-2000; 2000US-0233399P.
PR PR 14-SEP-2000; 2000US-0233400P.
PR PR 14-SEP-2000; 2000US-0233401P.
PR PR 14-SEP-2000; 2000US-0233463P.
PR PR 14-SEP-2000; 2000US-0233464P.
PR PR 14-SEP-2000; 2000US-0233465P.
PR PR 21-SEP-2000; 2000US-0234223P.
PR PR 21-SEP-2000; 2000US-0234274P.
PR PR 25-SEP-2000; 2000US-0234977P.
PR PR 25-SEP-2000; 2000US-0234978P.
PR PR 26-SEP-2000; 2000US-0235484P.
PR PR 27-SEP-2000; 2000US-0235834P.
PR PR 27-SEP-2000; 2000US-0235836P.
PR PR 29-SEP-2000; 2000US-0236327P.
PR PR 29-SEP-2000; 2000US-0236367P.
PR PR 29-SEP-2000; 2000US-0236368P.
PR PR 29-SEP-2000; 2000US-0236369P.
PR PR 29-SEP-2000; 2000US-0236370P.
PR PR 02-OCT-2000; 2000US-0237037P.
PR PR 02-OCT-2000; 2000US-0237038P.
PR PR 02-OCT-2000; 2000US-0237039P.
PR PR 02-OCT-2000; 2000US-0239935P.
PR PR 13-OCT-2000; 2000US-0239937P.
PR PR 20-OCT-2000; 2000US-0240960P.
PR PR 20-OCT-2000; 2000US-0241221P.
PR PR 20-OCT-2000; 2000US-0241785P.
PR PR 20-OCT-2000; 2000US-0241786P.
PR PR 20-OCT-2000; 2000US-0241787P.
PR PR 08-NOV-2000; 2000US-0241809P.
PR PR 08-NOV-2000; 2000US-0241826P.
PR PR 01-NOV-2000; 2000US-0244617P.
PR PR 08-NOV-2000; 2000US-02446474P.
PR PR 08-NOV-2000; 2000US-0244675P.
PR PR 08-NOV-2000; 2000US-0244676P.
PR PR 08-NOV-2000; 2000US-0244677P.
PR PR 08-NOV-2000; 2000US-0244678P.
PR PR 08-NOV-2000; 2000US-02446523P.
PR PR 08-NOV-2000; 2000US-02446524P.
PR PR 08-NOV-2000; 2000US-02446525P.
PR PR 08-NOV-2000; 2000US-02446526P.
PR PR 08-NOV-2000; 2000US-02446527P.
PR PR 08-NOV-2000; 2000US-02446528P.
PR PR 08-NOV-2000; 2000US-02446529P.

Query Match 43.4%; Score 49; DB 4; Length 378;
 Best Local Similarity 50.0%; Pred. No. 82;
 Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MKRMSLAAALTVGMLAAPVAT 24
 Db 40 MKRSKRIAAALTSLLTIVATAFAT 63

RESULT 31
 ABM50663 standard; protein; 378 AA.
 AC ABM50663;
 XX DT 20-OCT-2003 (first entry)
 XX DF Propionibacterium acnes predicted ORF encoded polypeptide #15339.
 XX KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
 XX immunostimulant; immune response; vaccine.
 OS Propionibacterium acnes.
 XX PN WO200303515-A1.
 PD 24-APR-2003.
 XX PF 11-OCT-2002; 2002WO-US032727.
 PR 15-OCT-2001; 2001US-00978825.
 XX PA (CORIXA CORP.
 XX PI Mitcham JL, Skeirly YAW, Persing DH, Bhatia A, Maisonneuve JL,
 Zhang Y, Wang S, Jen S, Iodes MJ, Benzon DR, Jones R, Carter D,
 Barth B, Vallieve-Douglass J;
 XX DR WPI; 2003-3B1789/36.
 XX N-FSDB; ACF64492.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 15339; 148pp; English.

The invention relates to an isolated polynucleotide (ACB64435-ACB64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotide (ABM3624-ABM64336) and to immunogenic fragments of P. acnes polypeptides. The invention encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide; a method and kit for detecting or determining the presence or absence of P. acnes in a patient and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences

CC the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 378 AA;

Query Match 43.4%; Score 49; DB 6; Length 378;
 Best Local Similarity 50.0%; Pred. No. 82;
 Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MKRMSLAAALTVGMLAAPVAT 24
 Db 40 MKRSKRIAAALTSLLTIVATAFAT 63

RESULT 32
 ABG2971 ID ABG29771 standard; protein; 895 AA.
 AC ABG29771;
 XX DT 18-FEB-2002 (first entry)
 XX DB Novel human diagnostic protein #29762.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 PD 11-OCT-2001.
 XX PP 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSEQ INC.
 XX PR Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 DR N-PSB; AAS93958.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 60130; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG31377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences

	X	Sequence 895 AA;	Score 49; DB 4; Length 895;				RESULT 24
Q		Query Match Score 43.4%; Best Local Similarity 47.6%; Matches 10; Conservative Matches 10; Unidentified.	Pred. No. 2.2e+02; Mismatches 6; Indels 5; Gaps 0;				ADJ34916 standard; protein; 405 AA.
	Y	3 RMKSLAAALTVAGMLAAPVATA 23					XX
b		671 RTLTMVAVTIASAILAAPPNA 691					XX
		RESULT 33					Xylanase from an environmental sample seq id 132.
	D	ADJ49642 standard; protein; 132 AA.					DT 22-APR-2004 (first entry)
	X	ADJ49642;					XX
	X	X					XX
	T	06-MAY-2004 (first entry)					XX
	X	Oil-associated gene related protein #1142.					PD 24-DEC-2003.
	X	X					XX
	R	oil-associated gene; transgenic; enhanced seed oil; vegetable oil.					PF 16-JUN-2003; 2003W0-US019153.
	X	X					XX
	S	Unidentified.					PR 14-JUN-2002; 2002US-0319299P.
	X	X					XX
	US2004025202-A1.						(DIVE-) DIVERSA CORP.
	X	X					PA PA
	05-FEB-2004.						PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
	X	X					PI Esteghlalian A;
	F	14-MAR-2003; 2003US-00389566.					XX
	X	X					DR WPI; 2004-099016/10.
	15-MAR-2002; 2002US-0365301P.						DR N-PSDB; ADJ34915.
	X	X					XX
	26-JUN-2002; 2002US-0391786P.						XX Novel xylanase recombinant polypeptide useful for improving textile
	X	X					PT texture, treating paper, eliminating microorganisms.
	26-JUN-2002; 2002US-0392018P.						XX
	X	X					PS Claim 60; SEQ ID NO 132; 570pp; English.
	(LAUTR.) LAURIE C. C.,						XX
	(RAV.) RAVANELLO M.						CC The invention describes an isolated or recombinant polypeptide (I),
	(SAVA.) SAVAGE T.						CC having 50% or more identity to 190 300-1200 residue amino acid sequences
	(LEDE.) LEDEAU J. R.						CC (S1), given in the specification, over a region of 100 or more residues
	(ROGE.) ROGERS J. A.						CC and the polypeptide as thermostable xylanase activity. (I) is useful for
	X	X					CC dough conditioning; beverage production; as a nutritional supplement in
	Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;						CC animal feed; reducing lignin in a wood or a wood product; and for
	WPI; 2004-142688/14.						CC eliminating and protecting animals from a microorganism comprising xylan
	X	X					CC acid (II) encoding (I) is useful for amplifying nucleic
	Novel recombinant DNA construct comprising a promoter functional in						CC acid encoding a polypeptide having a xylanase activity which involves
	plants operably linked to an oil-associated gene for producing transgenic						CC amplification of a template nucleic acid with a primer pair capable of
	plants.						CC amplifying (II) or its subsequence. (I) is useful for treating and
	X	X					CC preventing bacterial infection and fungal infection e.g. coccidioides.
	Example 3; SEQ ID NO 1646; 22pp; English.						CC This is the amino acid sequence of a xylanase protein isolated from an
	X	X					CC environmental sample.
	Sequence 405 AA;						XX
	SQ						SQ Sequence 405 AA;
							Query Match Score 42.1%; Best Local Similarity 47.8%; Matches 11; Conservative 11; Unidentified.
							DB 8; Length 405; Pred. No. 1.2e-02; Mismatches 6; Indels 0; Gaps 0;
							XX
	Y	7 LALALTYGAGMLAAPVATA 25					RESULT 35
		:: : : : :					ABU22871
		33 VSAAAPGGMVAAPVAGA 51					ID ABU22871 standard; protein; 998 AA.
							AC XX
							DT 19-JUN-2003 (first entry)
							XX
							XX Protein encoded by Prokaryotic essential gene #839.

XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Bordetella pertussis.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0312923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-1) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL,
XX Wall D, Trawick JD, Carr GI, Yamamoto R, Porsyth RA, Zyskind JW;
XX
XX WPI; 2003-023926/02.
XX N-ESDB; ACA22741.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 50795; 1766PP; English.

required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftb.wipo.int/pub/published_pct_sequences

XX Sequence 260 AA;

Query Match Score 47; DB 6; Length 260;
Best Local Similarity 50.0%; Pred. No. 1.1e+02; N mismatches 7; Indels 0; Gaps 0;

Qy 1 M K R M K S L A A L T V A G A M I L A P V 22
| : | : | : | : || |
Db 1 M R F G S L L A L S I T G A H A R A P V 22

RESULT 39

ABU21338 ABU21338 standard; protein; 409 AA.
XX AC ABU21338;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #6865.

XX Antisense: prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia fungorum.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 05-SEP-2001; 2001US-00348993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00672851.

PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; Wall D, Trawick JD, Carr GD, Yamamoto R, Forsyth RA, Xu HH; WPI: 2003-029526/02.

DR N-PSDB; ACA25208.

New antisense nucleic acids useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 49262; 1766PP; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SO Sequence 409 AA;

Query Match Score 47; DB 6; Length 409;
Best Local Similarity 61.1%; Pred. No. 1.8e+02; Mismatches 5; Indels 0; Gaps 0;

AC 3 RMKSLAAALTYAGAMIAA 20
| : || | : || : || |
DB 14 RTRSLAAALSIVASCMFMA 31

RESULT 40

AAB47297

ID AAB47297 standard; protein; 458 AA.
XX AC AAB47297;
XX DT 22-AUG-2001 (first entry)
XX DE PRO9912 polypeptide.

XX PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte; PRO1199; PRO1556; PRO4401; PRO10268; inhibition; stimulation; infiltration; mononuclear cell; eosinophil; erythema multiforme; polymorphonuclear neutrophil; PNN; antibody; immune-related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis; idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease; systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; asthma; immune-mediated renal disease; demyelination; central nervous system; Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia; chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis; granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity; inflammatory bowel disease; gluten-sensitive enteropathy; urticaria; Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis; psoriasis; atopic dermatitis; hypersensitivity pneumonitis; graft rejection; graft-versus-host disease.

XX Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..22 /label= Signal peptide
FT Protein 23..458 /label= Mature PRO9912
FT Modified-site 92..98 /label= N-myristoylation site
FT Modified-site 100..104 /label= N-glycosylation site
FT Modified-site 121..125 /label= N-glycosylation site
FT Modified-site 134..140 /label= N-glycosylation site
FT Modified-site 144..150 /label= N-myristoylation site

/label= N-myristoylation site
 146..150 /label= N-glycosylation site
 151..157 /label= N-myristoylation site
 /label= N-myristoylation site
 161..167 /label= N-myristoylation site
 168..172 /label= N-glycosylation site
 267..271 /label= N-glycosylation site
 /label= Leucine zipper pattern
 446..452 /label= N-myristoylation site
 WO200140465-A2.
 XX
 PD 07-JUN-2001.
 XX
 PR 10-NOV-2000; 2000WO-US030873.
 XX
 PR 30-NOV-1999; 99WO-US028313.
 PR 09-DEC-1999; 99US-0170262P.
 PR 23-DEC-1999; 99US-017059P.
 PR 20-JAN-2000; 2000US-017548P.
 PR 18-FEB-2000; 2000US-0177118P.
 PR 03-MAR-2000; 2000US-01804342.
 PR 30-MAY-2000; 2000WO-US014922P.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 24-AUG-2000; 2000WO-US023328.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 Hillian KJ, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2001-381384/40.
 N-PSDB; AAC85567.
 PR Isolated PRO polypeptide useful for treat or diagnose an immune-related disorder e.g. arthritis, asthma, allergy, diabetes or psoriasis.
 XX
 PA Claim 1; Fig 14; 124pp; English.
 XX
 CC The sequences given in AAB47291-99 show PRO polypeptides PRO1081, PRO1274 and PRO10272 stimulate the proliferation of T-lymphocytes and CC PRO119, PRO156, PRO4401, and PRO10268 inhibit the proliferation of T-CC lymphocytes. PRO1754 and PRO9912 act to enhance the infiltration of mononuclear cells, eosinophils or polymorphonuclear neutrophils (PMN) CC into the tissue of a mammal. The PRO cDNA's and antibodies which bind to them, are used to treat an immune-related disorder in a mammal. Such CC disorders include systemic lupus erythematosus, rheumatoid arthritis, CC osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, CC systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, CC immune-mediated renal disease, a demyelinating disease of the central or CC peripheral nervous system, idiopathic demyelinating polyneuropathy, CC Guillain-Barre syndrome, a chronic inflammatory demylinating CC polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic CC active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, CC sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive CC enteropathy, Whipple's disease, an autoimmune or immune-mediated skin CC disease, a bullous skin disease, erythema multiforme, contact dermatitis, CC psoriasis, an allergic disease, asthma, allergic rhinitis, atopic CC dermatitis, food hypersensitivity, urticaria, an immunologic disease of CC the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, CC hypersensitivity pneumonitis, a transplantation associated disease, graft CC rejection or graft-versus-host disease
 XX Sequence 458 AA;
 SQ

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